

NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N. meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (*ie.* substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins).

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (i) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

Expression systems

The *Neisseria menB* nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Reprtr*, 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl. Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected.

Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (alpha) α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412.

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alpha factor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCl/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guillermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

Bacteriol. 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; Pichia]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 Saccharomyces]; [Beach and Nurse (1981) *Nature* 300:706; Schizosaccharomyces]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; Yarrowia].

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular Neisserial protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular Neisserial protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a Neisserial sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An “origin of replication” is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A “mutant” sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an “allelic variant” of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

Antibodies

As used herein, the term “antibody” refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An “antibody combining site” is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. “Antibody” includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria* menB proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinitite virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, *eg.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *eg.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E.Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

F.Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin[®], and lipofectAMINE[®] are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

“Hybridization” refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

“Stringency” refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1 μg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/ μg . For a single-copy mammalian gene a conservative approach would start with 10 μg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/ μg , resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4\%[(G + C)] - 0.6(\% \text{formamide}) - 600/n - 1.5(\% \text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

Chromosomal DNA Preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl₃/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	(<i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	(<i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	(<i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	(<i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	(<i>Xho</i> I)
	<u>CCCGCTCGAG</u>	(<i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	(<i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	(<i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	(<i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	(<i>Xba</i> I)

5' or 3'-end primer tail: AAAGCATGC (*Sph*I) AAAAAAAGTCGAC (*Sal*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml NH₄OH, and deprotected by 5 hours incubation at 56°C. The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100µl or 1.0ml of water. The OD₂₆₀ was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10pmol/µl.

Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40µM of each oligonucleotide primer, 400-800µM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl₂), 2.5 units *TaqI* DNA polymerase (using

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5.

Digestion of PCR fragments

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H₂O or 10 mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260nm} and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

Cloning

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 μ l of NEB T4 DNA ligase (400 units/ μ l), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 μ l *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 μ l LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 μ l of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 μ g/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 μ l. 5 μ l of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20 μ l, that included 0.5 μ l T4 DNA ligase (400 units/ μ l, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100 μ l of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800 μ l LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200 μ l of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C in gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

GST-fusion proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M'') (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD_{280nm} of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD_{280nm} of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

His-fusion soluble proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

His-fusion insoluble proteins large-scale purification.

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD₂₈₀ of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

Purification of His-fusion proteins.

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni²⁺-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD_{280nm} of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD_{280nm} of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the $O.D_{280nm}$ indicated all the recombinant protein was obtained. 20 μ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

His-fusion proteins renaturation

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 μ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

Purification of proteins

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 μ l buffer M1 (PBS pH 7.2). 25 μ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

Mice immunisations

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

ELISA assay (sera analysis)

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD₄₉₀ was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 μ l of H₂O₂) were added to each well and the plates were left at room temperature for 20 minutes. 100 μ l of 12.5% H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD₄₉₀ value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD₄₉₀ of 0.4 was higher than 1:400.

FACScan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100 μ l bacterial cells were added to each well of a Costar 96 well plate. 100 μ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 μ l/well of blocking buffer in each well. 100 μ l of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 μ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

Bactericidal assay

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° (in according to T _m of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or
CTGCGCCCTGTGTAAAATCCCCT
- 919.2 (forward) ATCCTTCCGCCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCC
- 919.10 (reverse) TCGTTCCGGCGGGGTCGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 1: Oligonucleotides used for PCR for Examples 2-10

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTGCGAAA <SEQ ID 3032>	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTGTGCC <SEQ ID 3036>	XhoI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

designated sequences being compared, the designated sequence controls and is the actual sequence being compared.

ORF: contig:

279 gnm4.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3039>:

m279.seq

1	ATAACGCGGA	TTTGC GGCTG	CTTGATTTC	ACGGTTTTCA	GGGCTTCGGC
51	AAGTTTGTCTG	GCGGCGGGTT	TCATCAGGCT	GCAATGGGAA	GGTACGGACA
101	CGGCGACGCG	CAGGCGCGT	TTGGCACCCG	CTTCTTTTGC	GGCAGCCATG
151	GCGCGTCCGA	CGGCGGCGGC	GTTCCTTCGA	ATCACGATT	GTCCGGGTGA
201	GTTGAAGTTG	ACGGCTTCGA	CCACTTCGCT	TTGGGCGGCT	TCGGCAACAA
251	TGGCTTTAAC	CTGCTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	GGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	TCAATGCGCC	GGCGGCAACG	AGTGCGGTGT
401	ATTTCGCGAG	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCATAAATAG				

This corresponds to the amino acid sequence <SEQ ID 3040; ORF 279>:

m279.pep

1	ITRICGCLIS	TVFRASASLS	AAGFIRLQWE	GTDTGSGRAR	LAPASLAAAM
51	ARPTAAALPA	ITICPGELKL	TASTTSLWAA	SAQMALTCS	SKPRIAAIAP
101	TPCGTADCIS	SARRRTSLTA	SAKFNAPAAT	SAVYSPRLCP	ATAAGVLPPA
151	SK*				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3041>:

g279.seq

1	atgacgcgga	tttgcggtcg	cttgatttca	acggttttga	gtgtttcggc
51	aagtttgtcg	gcggcggtt	tcatcaggct	gcaatgggaa	ggaacggata
101	ccggcagcgg	cagggcgcgt	ttggctccgg	cttctttggc	ggcagccatg
151	gtgcgtccga	cggcggcggc	gttgctgcga	atcacgactt	gtccgggcga
201	gttaagttg	acggcttcga	ccacttcgcc	ctgtgcggat	tccgcaacaa
251	ttgcctgac	ctgttcattc	tccaaaccca	aaatggccgc	cattgcgcct
301	acgccttgcg	gtacggcgga	ctgcatcagt	tccggcgcga	ggcggacgag
351	tttgacggca	tccgcaaaat	ccaatgcttc	ggcggcgaca	agcgcggtgt
401	attcgcctga	gctgtgtccg	gcaacggcgg	caggcgtttt	gccgcccatc
451	tccaaataq				

This corresponds to the amino acid sequence <SEQ ID 3042; ORF 279.ng>:

q279 . pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSA SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA : : : : : : :					
g279	MTRICGCLISTVLVSASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMVRPTAAALPA 10 20 30 40 50 60					

```
a279.seq
1  ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNA GGGCTTCGGC
51  GAGTTTGTCG GCGGCGGGTT TCATGAGGCT GCAATGGGAA GGTACNGACA
101 CNGGCAGCGG CAGGCGCGCT TTGGCGCCGG CTTCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGC ATTGCCTGCA ATCAGCACTT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACCTTCAT CTCGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GGCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCCGCT
451 TCCGAATAG
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a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	<u>ARSTAAALPA</u>	<u>ITTCPGELKL</u>	<u>TASTTSSCAD</u>	<u>SAQICFTCSS</u>	<u>SKPRIAAIAP</u>
101	<u>TPCGTADCIS</u>	<u>SARXRTSLTA</u>	<u>SAKSNAPAAAT</u>	<u>SAVYSPXLCP</u>	<u>ATAAGVLPPA</u>
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA					
	: : :					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	:					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
	:					
a279	SAKSNAAPAATSAVYSPXLCPPATAAGVLPPASEX					
	130	140	150			

```
m519.seq (partial)
1  ..TCCGTTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAG ACTTGGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAATTACT GCCGCAACGC AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
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m519.pep      (partial)
  1  ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAAQ
101  AVNASMAQEI ARINRAKGEA ESLRLVAEN AEAIRQIAAA LQTGGADAV
151  NLKIAEOVVA AFNNLAKESN TLIIPANVAD IGSLLISAGMK IIDSSKTAK*
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g519.seq					
1	atggaatttt	tcaattatctt	gttggcagcc	gtcgccggtt	tcggcttcaa
51	atcctttgtc	gtcatcccc	agcaggaaagt	ccacgttgtc	gaaaggctcg
101	ggcgtttcca	tcgcgccctg	acggccggtt	tgaatatattt	gattccctt
151	atcgaccgcg	tcgcctaccg	ccattcgctg	aaagaaaatcg	ctttagacgt
201	accgagccag	gtctgcatac	cgcgcgataa	tacgcaattg	actgttgacg
251	gcatactcta	tttccaagta	accgatccca	aactcgccctc	atacggttcg
301	agcaactaca	ttatggcaat	tacctagctt	gccc aaacga	cgtctgcgttc
351	cgttatcggg	cgtatggagt	tggacaaaac	gtttgaagaa	cgcgacgaaa
401	tcaacagtac	cgtcgtctcc	gcctcgaatg	aagccgcggg	ggcttgggggt
451	gtgaaagtcc	tccgttacga	aatcaaggat	ttggttcgcg	cgcgaagaat
501	ccttcgcgca	atgcaggcac	aaattaaccg	cgaacgcgaa	aaacgcgcgc
551	gtattgccga	atccgaaggc	cgtaaaaatcg	aacaaatcag	ccttgccagt
601	ggtcagcgtg	aagccgaaat	ccaacaatcc	gaagcgtagg	ctcaggtctgc
651	ggtcaatcgc	tccaatgcgc	agaaaaatcgc	ccgcatcaac	cgcgcgcaaag
701	gcgaagcgga	atccctgcgc	cttgttgccg	aagccaatgc	cgaagccaac
751	cgtcaaattg	cgcgcgcctt	tcaaacccaa	agcggggcgg	atgcggtcaa
801	tctgaagatt	gcgggacaat	acgttaccgc	gttcaaaaaat	cttgccaaag
851	aagacaatac	gcggattaag	cccgcceaag	ttgccgaaat	cgggaaccct
901	aattttcggc	ggcatgaaaa	attttcgcca	gaagcaaaaa	cggccaaata
951	a				

g519.pep

1	<u>MEFFIILLAA</u>	<u>VAVFGFKSFV</u>	VI PQQEVHVV	ER LGRFHRAL	TAGLNILIPF
51	IDRVAYRHSL	KEIPLDVP SQ	VCITRDNTQL	TV DGI IYFQV	TD PKLAS YGS
101	SNYIMAITQL	AQTTLRSVIG	RMELDKTFEE	RDEINSTVVS	ALDEAAGAWG
151	VKVLRYEIKD	LVPPQEILRA	MQAQITAERE	KRARIAESEG	RKIEQINLAS
201	GQREAEIQQS	EGEAQA AVNA	SNAEKIARIN	RAKGEAESLR	LVAEANA EAN
251	RQIAAALQTP	SGADAVNLKI	AGQYVTA FKN	LAKEDNRIK	PAKVAEIGNP
301	NFRREHKFSP	EAKTAK*			

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m519/g519
m519.pep
g519
m519.pep

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g519      |||||:|||||
          GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEG RKIEQINLASGQREAE
          150      160      170      180      190      200

m519.pep      100      110      120      130      140      150
          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANA EAIRQIAAALQTQGGADAV
g519      |||||:|||||
          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV
          210      220      230      240      250      260

m519.pep      160      170      180      190      200
          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL- ISAGMKIIDSSKTAK
g519      |||||:|||||
          NLKIAGQYVTAFAKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSPEAKTAK
          270      280      290      300      310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3049>:

```

a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATGCG TCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAG
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAAATA

```

This corresponds to the amino acid sequence <SEQ ID 3050; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKFSV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGAEQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

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m519/a519 ORFs 519 and 519.a showed a 99.5% identity in 199 aa overlap

```

m519.pep      10      20      30
          SVIGRMELDKTFEERDEINSTVVVAALDEAA
a519      |||||:|||||
          YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100      110      120      130      140

m519.pep      40      50      60      70      80      90
          GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEG RKIEQINLASGQREAE
a519      |||||:|||||
          GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEG RKIEQINLASGQREAE
          150      160      170      180      190      200

          100      110      120      130      140      150

```

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m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILLVA VAVFGFSKV VIPOQEVHVV ERLGRFHRAL TAGLNILIPF
51 IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GOREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51 ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAATATA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep
1 MEFFFIILLAA VAVFGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
m519-1	MEFFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq
1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA

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401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGT CAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVF GFKSFV VIPQ QEVHV V ERLGRFHRAL TAGLNILIPF
51  IDR VAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPK LASYGS
101 SNYIMAITQL AQTT LRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKV LRYEIKD LVPPQEILRS MQAQITAE RE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EG EAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

a519-1.pep	MEFFIILLAAVVVF	GFKSFV	VIPQ	QEVHV	V	ERLGRFHRAL	TAGLNILIPF	IDR VAYRHSL
m519-1	MEFFIILLVAVAV	GFKSFV	VIPQ	QEVHV	V	ERLGRFHRAL	TAGLNILIPF	IDR VAYRHSL
a519-1.pep	KEIPLDVPSQVCITRDNTQL	TVDGIIFYQV	TDPK LASYGS	SNYIMAITQL	AQTT LRSVIG			
m519-1	KEIPLDVPSQVCITRDNTQL	TVDGIIFYQV	TDPK LASYGS	SNYIMAITQL	AQTT LRSVIG			
a519-1.pep	RMELDKTFEERDEINSTVVS	ALDEAAGAWG	VKV LRYEIKD	LVPPQEILRS	MQAQITAE RE			
m519-1	RMELDKTFEERDEINSTVVA	ALDEAAGAWG	VKV LRYEIKD	LVPPQEILRS	MQAQITAE RE			
a519-1.pep	KRARIAESEGRKIEQINLAS	GQREAEIQ	QSEGEAQA	AVNASNAEKIARIN	RAKGEAESLR			
m519-1	KRARIAESEGRKIEQINLAS	GQREAEIQ	QSEGEAQA	AVNASNAEKIARIN	RAKGEAESLR			
a519-1.pep	LVAEANA EAI	RQIAAALQTQ	GGADAVNLKI	AEQYVAAFNN	LAKESNTLIM	PANVADIGSL		
m519-1	LVAEANA EAI	RQIAAALQTQ	GGADAVNLKI	AEQYVAAFNN	LAKESNTLIM	PANVADIGSL		
a519-1.pep	ISAGMKIIDSSKTAKX							
m519-1	ISAGMKIIDSSKTAKX							

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAAATGAAG GAACAGGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCAATGCAGGC AGTGTATGAC GGAAAGAAAG TCAAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGACCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGGC
301 CTGCAATACA AAATCACCAA ACAGAGCGAA GGCAAACAGC CGACCAAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTAATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551 GCGACAAAAA CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

m576.pep.. (partial)

1	..MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ
51	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK	GEAFLKENAA	KDGVKTTASG
101	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN	GGPVTFPLSQ
151	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFVDVKLV
201	KIGAPENAPA	KQPAQVDIKK	VN*		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

g576.seq.. (partial)

1	..atgggcggtgg	acatcgggacg	ctccctgaaa	caaatgaagg	aacaggggcgc
51	ggaaatcgat	ttgaaagtct	ttaccgatgc	catgcaggca	gtgtatgacg
101	gcaaagaat	caaaatgacc	gaagagcagg	cccaggaagt	gatgatgaaa
151	ttcctgcagg	agcagcaggc	taaagccgta	gaaaaacaca	aggcggatgc
201	gaaggccaac	aaagaaaaag	gcgaagcctt	cctgaaggaa	aatgccgcgcg
251	aagacggcgt	gaagaccact	gcttcgcgtc	tgcagtacaa	aatcaccaaa
301	cagggtgaag	gcaaacagcc	gacaaaagac	gacatcgta	ccgtggaata
351	cgaaggccgc	ctgatcgacg	gtaccgtatt	cgacagcagc	taaggcaacg
401	gcggcccggc	caccttccct	ttgagccaag	tgattccggg	ttggaccgaa
451	ggcgtagcgc	ttctgaaaga	aggcggcgaa	gccacgttct	acatcccgtc
501	caacctttgc	taccgcgaac	agggtgcggg	cgaaaaaatc	ggtocgaacg
551	ccacttttgt	atttgacgtg	aaactgtgtc	aaatcggcgc	accggaaaac
601	gcgcccgcga	agcagccgga	tcaagtcgac	atcaaaaaag	taaattaa

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

g576.pep.. (partial)

1	..MGVDIGRSLK	QMKEQGAEID	LKVFTDAMQA	VYDGKEIKMT	EEQAQEVMMK
51	FLQEQQAKAV	EKHKADAKAN	KEKGEAFLKE	NAAEDGVKTT	ASGLQYKITK
101	QGEGKQPTKD	DIVTVEYEGR	LIDGTVFDSS	KANGGPATFP	LSQVIPGWTE
151	GVRLLEKEGE	ATFYIPSNLA	YREQGAGEKI	GPNATLVFDV	KLVKIGAPEN
201	APAKQPDQVD	IKKVN*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

m576.pep 10 20 30 40 50 60
 MQQASYAMGVDIGRSLKQMKEQGAIEDLKVFTEAMQAVYDGKEIKMTEEQAQEVMMKFLQ
 |||||

```

g576          MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQ
                10      20      30      40      50

                70      80      90      100     110     120
m576.pep      EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGGKOPTKDDIV
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g576          EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGGKOPTKDDIV
                60      70      80      90      100     110

                130     140     150     160     170     180
m576.pep      TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g576          TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
                120     130     140     150     160     170

                190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN*
                ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g576          QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN*
                180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGC GGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1   MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

                10      20      30
m576.pep      MQQASYAMGVDIGRSLKQMKEQGAEIDLKV
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a576          CGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGVDIGRSLKQMKEQGAEIDLKV
                30      40      50      60      70      80

                40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                90      100     110     120     130     140

```

	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
a576	KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
	150	160	170	180	190	200
	160	170	180	190	200	210
m576.pep	VIPGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFVDVKLVKIGAPENAPA					
a576	VILGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFVDVKLVKIGAPENAPA					
	210	220	230	240	250	260
	220					
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

m576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCCGCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	GCAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCTCAGGAAG	TCATGATGAA	ATTCCTTCAG	GAACAACAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
451	CTGCAATACA	AAATCACCAA	ACAGGGCGAA	GGCAAACAGC	CGACCAAAGA
501	CGACATCGTT	ACCGTGGAAAT	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	TCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACAG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTC	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
701	GCGACAAAAT	CGGTCCGAAC	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
801	CATCAAAAAA	GTAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

m576-1.pep

1	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAAASSA	QGDTSSIGST
51	MQQASYAMGV	DIGRSLKOMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ
101	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK	GEAFLKENAA	KDGVKTTASG
151	LQYKITQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN	GGPVTFPLSQ
201	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFVDKLV
251	KIGAPENAPA	KQPAQVDIKK	VN*		

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

g576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTGCCGCG	CAGGGCGACA	CCTCTTCAAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	AATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	ACAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGATG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GGCCAGGAAG	TGATGATGAA	ATTCCTGCAG	GAGCAGCAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGATG	CGAAGGCCAA	CAAAGAAAAA	GGCGAAGCCT
401	TCCTGAAGGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGT
451	CTGCAGTACA	AAATCACCAA	ACAGGGTGAA	GGCAAACAGC	CGACAAAAGA
501	CGACATCGTT	ACCGTGGAAAT	ACGAAGGCCG	CCTGATTGAC	GGTACCGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	CCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACGG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTC	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG

701 GCGAAAAAAT CCGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKOMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPDQVDIKK VN*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASAA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASAA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
	70	80	90	100	110	120
g576-1.pep	DIGRSLKOMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKOMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGPN
m576-1	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGPN
	190	200	210	220	230	240
	250	260	270			
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VNX		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VNX		
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
 251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAATGAC CGAAGAGCAG
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
 451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
 551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
 601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep
 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq
 1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
 101 CATCCGTCAT CAACGGCCCG GACCGCCCG TCGGCATCCC CGACCCCGCC
 151 GGAACGACGG TCGGCGCGG CGGGGCCGTC TATACCGTTG TACCGCACCT
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATT TCGCCAAAAGC CTGCAATCCT
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
 301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT
 351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

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451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATAACGCCG ACCTCTCCcG ATTCCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCCTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAATCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

```

m919.pep
1 MKKYLFRAL YGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPQR LAEVLGQNPS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

```

g919.seq
1 ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51 CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGCGCG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATAACGCCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaggCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcg tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCat cggatagcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcata aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGCGCGA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

```

g919.pep
  1 MKKHLLRSAL YGIAAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
 51 GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGLG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTGYVWQL LPNGMKPEYR P*

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ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

m919.pep	10	20	30	40	50	60
	MKKYLFRALYGI AAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
g919	MKKHLLRSALYGI AAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
m919.pep	70	80	90	100	110	120
	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKQFFER					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKRFFER					
	70	80	90	100	110	120
m919.pep	130	140	150	160	170	180
	YFTPQVAGNGSLAGTVTGYIEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA					
g919	YFTPQVAGNGSLACTVTGYIEPVLKGDGRRTARFPIYGI PDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
	KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYI FFFRELAYSNDGPVGLGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYI FFFRELAYSNDGPVGLGTPLMGEYAGA					
	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420

	430	440
m919.pep	QKTTGYVWQLLPNGMKPEYRPX	
g919	QKTTGYVWQLLPNGMKPEYRPX	
	430	440

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGGCATCG CCGCCGCCAT
51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCGCC
151 GGAACGACGG TCGGCGCGCG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CTTTCAAAC CCCCCTCCAT TCCGTTCAGG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGCACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 TCCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCA ATTCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCAGTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAATC
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDFA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGONPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

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m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

	10	20	30	40	50	60
m919.pep	MKKYLFRALYGLIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
a919	MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER					
a919	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER					
	70	80	90	100	110	120

m919.pep	130	140	150	160	170	180
	YFTPWQVAGNGSLAGTVTGYEYVVLKGD	DRRTAQARFPIYGIPDDFISVPLPAGLRSGKA				
a919	130	140	150	160	170	180
	YFTPWQVAGNGSLAGTVTGYEYVVLKGD	DRRTAQARFPIYGIPDDFISVPLPAGLRSGKA				
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
a919	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSI	GRYMADKGYL				
a919	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSI	GRYMADKGYL				
m919.pep	310	320	330	340	350	360
	KLQGTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL	AGSSNDGPVGALGTPLMGEYAGA				
a919	310	320	330	340	350	360
	KLQGTSMQGIKAYMQQNPRQRLAEVLGQNPSYIFFREL	TGSSNDGPVGALGTPLMGEYAGA				
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
a919	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
m919.pep	430	440				
	QKTTGYVWQLLPNGMKPEYRPX					
a919	430	440				
	QKTTGYVWQLLPNGMKPEYRPX					

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATAACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTTCGCAC
701 AACGCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACCGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```

1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
151 XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3077>:

g121.seq

```

1 ATGGAAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51 GGCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGACACGC CTTTACCCCT TACCTGACC GGTTCGCCCG CAAATTGCTG
151 GATTGTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCCGAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATAACG TTGCCGATTT
351 GCCGCTGCTG GCGGAACTGa cgcggatttt TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCCTCTT
451 CACGAAGCCC TGTTCCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGCGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAAacggt gcAAAGgcgg cacAAGGCAA
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac Tgtttgccc AAattggctc
751 gaaacctAcc ttgacggcgg cgaaccgca tacgacgtat tgcggacgct
801 ttcccgattc accgcgcaaa ccgTttggga cgcggtctca CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATttg
1001 cgtggttggc GGCGTGTGG ATTAACGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGCG CATCCAAACC GTGTATTCTG GGCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3078; ORF 121.ng>:

g121.pep

```

1 METQLYIGIM SGTSMGADA VLVRMDGGKW LGAEGHAFTP YPDRLLRRKLL
51 DLQDTGTDEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVWDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	: : : : :					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	: : : : :					

```

g121      HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
           70      80      90      100      110      120
           130      140      150      160      170      180
m121.pep  XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAPFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130      140      150      160      170      180
           190      200      210      220      230      240
m121.pep  XXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190      200      210      220      230      240
           250      260      270      280      290      300
m121.pep  GRELFAINWLETYLDGGENRYDVLRTLRSRFTAQTVCDVSHAAADARQMYICDGGIRNPV
           | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
g121      GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVWDVSHAAADARQMYICGGGIRNPV
           250      260      270      280      290      300
           310      320      330      340      350      360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
           | | | | | : | | | | | | | | | | | | | | | | | | | | | |
g121      LMADLAECFGTRVSLHSTAE LNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           310      320      330      340      350      360

m121.pep  XAGYYYY
           | | | | |
g121      GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCGGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAAGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATT CCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCTGACACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCTG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GGCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSPF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMADLAECFG TRVSLHSTAE LNLDPOWVEA AAFAWMAACW VNRI PGSPHK
 351 ATGASKPCIL GAGYYY*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

m121.pep	10	20	30	40	50	60
	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTYPYGRLLRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTYPYGRLLRQLLDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	70	80	90	100	110	120
	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQDLADLPLL					
a121	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHYSYVQLADLPLL					
	70	80	90	100	110	120
m121.pep	130	140	150	160	170	180
	XX					
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121.pep	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRI PGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPOWVEA AAFAWMAACWVNRI PGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
a121	GAGYYYYX					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TGCGGCCGCG GGACAAGGCG CGCCACTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCCGCGA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGGACGCA CCCGCTTCG
551 GCTTCGACAC AGGCGCGGCG AATATGCTGA TGGACGCGTG GACGACGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCG TATTTCGCAC
701 AAAAAACCCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGACGCG

```



```

851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
  1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRRLRRQLL
 51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSR TAQTVCAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPOWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEHGAFTPYPGRLRRQLLDLQDTGADEL					
	: : : : :					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEHGAFTPYPDRLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYISQLADLPLL					
	: : : : :					
g121	HRSRILSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPHEGYISQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA					
	: : : : :					
g121	AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	: : : : :					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVCAVSHAAADARQMYICGGGIRNPV					
	: : : : :					
g121	GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVWDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	: : : : :					
g121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121-1.pep	XAGYYYYX					
g121	GAGYYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
  1 ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCCGCCTTCG
551 GCTTCGACAC AGGACCGGCG AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGCGAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCATTTC ACCGCGCAAA CCGTTTTTCA CGCCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGCGAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAAGGCC GCCGCGTTTC
1001 CATGGATGGC GCGTGTGTTG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

```

a121-1.pep
  1  METQLYIGIM SGTSMDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMDLAECFG TRVSLHSTAE LNLDPQWVEA AFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
a121-1	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
m121-1.pep	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPHEHYSIQIQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPHEHYSYSVQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPHEHYSIQIQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPHEHYSYSVQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	AERTQIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121-1.pep	AERTQIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGPNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGPNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFCDVASHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFCDVASHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLD	PQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL				
a121	LMADLAECFGTRVSLHSTAE	NLDLPQWVEAAFAWMAACWVNRIPGSPHKATGASKPCIL				
	310	320	330	340	350	360

m121-1.pep	XAGYYYY
a121	GAGYYYY

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```
m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACC CGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACTCA ACTGCGTCGC CGACACGCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAAATC AACCAC
1  TACGCCAGCG AAAAACTGCG CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TayTTCCcyG TCGGCAAwGT ATTAAACGGA CTGTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGTC
151 TGGCACAAAG ACGTGCCTA TTKTGAATTG CAACAAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTaka ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAATAA TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CGGCATGTTC yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTCGCCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGGCCG CGAACCAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

```
m128.pep (partial)
1  MTDNALHLHG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLPSPAKTKL NH

//
1  YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTPVP
51  WHKDVRXYEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSDGTL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHS GF DNAV*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACatca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACGCTTCCC CCGCACAAAA AACCAAGCTC GATCAGCACC
401 TGCGCGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 CCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGcaaaa cTGCTCGGCT TAAAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 TCTCGCCCGC GAACACCTCG GTCTCGCCGA CCCGAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTTCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGActaca AAGGCCGCGC CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAACggcgtA GAATGGGACG CGGTGGAAC GCCCAGCCAG
1501 TTTATGGAAG ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCCTGCCGAA AGAACTCTTC GACAAAAATGC
1601 TcgCGCCAA AAACCTCCAG CGCGGTATGT TCCTCGTCCG GCAAAATGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGCAAG CTATTACAGC TACGCATGGG CCGAAGTCct
1851 CAGCACCGAT GCCTACGCCG CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctCCCGCAGC
1951 gcgGCGGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTGCGC CAaagcggT TCGACAACGC gGcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1  MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERTLGIT ERVGRWGVV SHLNSVVDTP ELRAVYNELM PEITVFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAG
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFIHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSL YAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRWFQ EILAVGGSRS

```

651 AAESFKAFRG REPSIDALLR QSGFDNAA*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)
from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHLHLLTQVDELGV					
m128	GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSEDEGRKLNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDEGRKLNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEIILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEIILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330

```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1   ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTACG CGACACGCCG GAAGCTGCGG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCACGATC
401 TGCGCGATTT CGTCCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACGCGAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTTCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTC ACGGCGACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCGCGGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1   MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

```

551 FALFDMMIYS EDDEGR LKNW QQVLD S VRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYA AFEESDD VAATGKRWFQ EILAVGGSRS
 651 AAESFKA FRG REPSIDALLR HSGFDNAA*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT					
a128	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT					
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	130	140	150	160	170	180
	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128.pep	-----					
a128	190	200	210	220	230	240
	FDDAAPLAGIPEDALAMFAAAAQSEGKTYGKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
m128.pep	-----					
a128	250	260	270	280	290	300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVNLFLHDL					
m128.pep						140
						YASEKLREAKYAFSETXVKKYFPVGX
a128	310	320	330	340	350	360
	ARRAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTVPVVHKDVRYXELQQNGEXIGGVYMDLYAREGKRGAWM					
a128	370	380	390	400	410	420
	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQQNGETIGGVYMDLYAREGKRGAWM					
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	430	440	450	460	470	480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWD AVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLA AKNFQ					
a128	490	500	510	520	530	540
	ELGVSGINGVEWD AVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLA AKNFQ					
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLD S VRKKVAVIQPPEYNRFALSFGHIF					
a128	550	560	570	580	590	600
	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLD S VRKEVAVVRPPEYNRFANSFGHIF					

```

          400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

          460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3091>:

```

m128-1.seq
1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTGCG CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACACGATC
401 TGC CGGATT CGTCTCAGC GCGCGGAAC TGCCGCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 ACACTACCTC GCCGTATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAACTG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC GTTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGCGGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC ACCCGTCGGC
1351 GGCAGGGAAG CCCGCCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CGGTGGAAT GCCAGCCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTCCAA CGCGGCATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCCGTCA
1751 TCCAGCCGCC CGAATACAAC CGCTTCGCC TGAAGCTTCG CCACATCTTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGC CGCGAACCGA GCATAGACGC
2001 ACTTTGCGC CACAGCGGTT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

```

m128-1.pep.
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI

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101  GDIELYNRF  KTIKNSPEFD  TLSPAQKTKL  NHDLRDFVLS  GAELPPEQQA
151  ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201  AAQSESKTGY  KIGLQIPHYL  AVIQYADNRE  LREQIYRAYV  TRASELSDDG
251  KFDNTANIDR  TLANALQTAK  LLGFKNYAEL  SLATKMADTP  EQVLNFLHDL
301  ARRAKPYAEK  DLAEVKAFAR  ESLNLADLQF  WDLGYASEKL  REAKYAFSET
351  EVKKYFPVGK  VLNGLFAQIK  KLYGIGFTEK  TVPVVHKDVR  YFELQQNGET
401  IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFS  DGTLLQLPTAY  LVCNFAPPVG
451  GREARLSHDE  ILILFHETGH  GLHLLLTQVD  ELGVSGINGV  EWDAVEGPSQ
501  FMENFVWEYN  VLAQMSAHEE  TGVPLPKELF  DKMLAAKNFQ  RGMFLVRQME
551  FALFDMMIYS  EDDEGRLLKNW  QQVLDSVRKK  VAVIQPPEYN  RFALSFGHIF
601  AGGYSAGYYS  YAWAEVLSAD  AYAAFEESDD  VAATGKRWFQ  EILAVGGSRS
651  AAESFKAFRG  REPSIDALLR  HSGFDNAV*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1  ATGATTGACA  ACGCACTGCT  CCACTTGGGC  GAAGAACCCC  GTTTTAATCA
51  AATCAAAACC  GAAGACATCA  AACCCTGGCT  CCAAACCGCC  ATCGCCGAAG
101 CGCGCGGACA  AATCGCCGCC  GTCAAAGCGC  AAACGCACAC  CGGCTGGGCG
151 AACACCGTCG  AGCGTCTGAC  CGGCATCACC  GAACGCGTCG  GCAGGATTGT
201 GGGCGTCGTG  TCCCCTCTCA  ACTCCGTCGT  CGACACGCCC  GAACTGCGCG
251 CCGTCTATAA  CGAACTGATG  CCTGAAATCA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAACTGTA  CAACCGCTTC  AAAACCATCA  AAAATTCCCC
351 CGAATTGCA  ACGCTTTCCC  CCGCACAAAA  AACCAAGCTC  GATCACGACC
401 TGCGCGATTT  CGTATTGAGC  GGCGCGGAAC  TGCCGCCCGA  ACGGCAGGCA
451 GAACTGGCAA  AACTGCAAAC  CGAAGGCGCG  CAACTTTCCG  CCAAATCTCT
501 CCAAACGTC  CTAGACGCGA  CCGACGCGTT  CGGCATTAC  TTTGACGATG
551 CCGCACCGCT  TGCCGGCATT  CCCGAAGACG  CGCTCGCCAT  GTTTGCCGCC
601 GCCGCGCAA  GCGAAGGCAA  AACAGGTTAC  AAAATCGGCT  TGCAGATTCC
651 GCACTACCTT  GCCGTTATCC  AATACGCGCG  CAACCGCGAA  CTGCGCGAAC
701 AAATCTACCG  CGCCTACGTT  ACCCGTGCCA  GCGAACTTTC  AAACGACGGC
751 AAATCGACA  ACACCGCAA  CATCGACCGC  ACGCTCGAAA  ACGCATTGAA
801 AACCGCCAAA  CTGCTCGGCT  TTAAAAATTA  CGCCGAATTG  TCGCTGGCAA
851 CCAAATGGC  GGACACGCCC  GAACAGGTTT  TAAACTTCCT  GCACGACCTC
901 GCCGCGCGCG  CCAAACCTTA  CGCCGAAAAA  GACCTCGCCG  AAGTCAAAGC
951 CTTCGCCCCG  GAACACCTCG  GTCTCGCCGA  CCCGCAGCCG  TGGGACTTGA
1001 GCTACGCCG  CGAAAACTG  CGCGAAGCCA  AATACGCATT  CAGCGAAACC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGCGAAA  GTTCTGGCAG  GCCTGTTCGC
1101 CCAAATCAA  AAATCTACG  GCATCGGATT  CGCCGAAAAA  ACCGTTCCCG
1151 TCTGGCACA  AGACGTGCGC  TATTTTGAAT  TGCAACAAAA  CGGCAAAACC
1201 ATCGGCGGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AACGCGGCGG
1251 CGCGTGGATG  AACGACTACA  AAGCGCGCCG  CCGCTTTGCC  GACGGCACGC
1301 TGCAACTGCC  CACCGCTTAC  CTCGTCTGCA  ACTTCGCCCC  GCCGTCGCG
1351 GGCAAGAAG  CGCGTTTAAG  CCACGACGAA  ATCCTCACCC  TCTTCCACGA
1401 AACCGCCAC  GGAATGCACC  ACCTGCTTAC  CCAAGTGGAC  GAACTGGGCG
1451 TGTCCGGCAT  CAACGGCGTA  AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG  EEPFRNQIKT  EDIKPAVQTA  IAEARGQIAA  VKAQHTGWA
51  NTVERTLGIT  ERVGRIWGVV  SHLNSVVDTP  ELRAVYNELM  PEITVFTEI
101  GDIELYNRF  KTIKNSPEFA  TLSPAQKTKL  DHDLRDFVLS  GAELPPERQA
151  ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201  AAQSEGKTGY  KIGLQIPHYL  AVIQYAGNRE  LREQIYRAYV  TRASELSNDG
251  KFDNTANIDR  TLENALKTAK  LLGFKNYAEL  SLATKMADTP  EQVLNFLHDL
301  ARRAKPYAEK  DLAEVKAFAR  EHLGLADPQP  WDLSYAGEKL  REAKYAFSET
351  EVKKYFPVGK  VLAGLFAQIK  KLYGIGFAEK  TVPVVHKDVR  YFELQQNGKT
401  IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFA  DGTLLQLPTAY  LVCNFAPPVG
451  GKEARLSHDE  ILTLFHETGH  GLHLLLTQVD  ELGVSGINGV  K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSONVL DATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSONVL DATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKSTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADQPWDL SYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCGGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCACGATC
401 TGC GCGATT TCGTCTCAGC GCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAC CGAAGGCGCG CAACTTTCG CCAAATTCTC

```

```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCCTG TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATAA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTTCG
1101 CCAAATCAAA AAACCTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGAAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAACCTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCCGCTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCGGCCA
1901 CAGGCAAACG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGW
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTYG KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMATDP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDVAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSR
651 AAESFKAERG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          |||
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90      100     110     120
a128-1.pep ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          |||
m128-1      ERVGRWGVVSHLNSVADTPELRVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90      100     110     120

          130     140     150     160     170     180

```

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGAGEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDSVRKKAQVIQPEYNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

```

1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GGCAGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCGCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCCGAcA GCCGcyTCAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pep..

```

1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3099>:

g206.seq

```

1  atgttttccc ccgacaaaac ccttttcctc tgtctcggcg cactgctcct
51  cgccctcatgc ggcacgacct ccggcaaaaca ccgccaacccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcggcgagca gcaccgcaac cggccttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcggaat tcattccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttgga gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	:					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRPTARDMAAASRKIPDSRXKAGD					
	:					
g206	LGLIGTPYKWGGSSTATGFDCSGMIQLVYKNALNVKLPRPTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	: :					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPGSGKTIKTEKLSTPFYAKNYLGAHTFFTE					

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCCTTAA
351 GGCCGGCGAC CTGCTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP TARDMAAASRK IPDSRLKAGD					
a206	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GGCGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCCCT GTTGTCTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GGCGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCCGCGTT
551 CTTCAGATCC CATCCCCGCG TCAAACCCTG CACCTGCGAA TGGCGGTAGC
```

```

601 AATTTTGGAA GGGTTGATT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAAT CAGAATTTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCGGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCGAG
1201 TTTGCCGCAA AAGTCGATT CGGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGGCGAT GATTTGCATA TGGGTACGCA AAAATTCAA GCGGCCATCG
1301 ATGGAACCG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGCGG ATTCGGCGTG TTTGCCGCGA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

m287. pep

```

1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNNGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDF NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQNAAGTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRGVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRRS
301 ARSRRSLPAE MPLIPVNOAD TLIVDGEAVS LTGHSNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTOKEK AAIDGNNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

g287. seq

```

1 atgttttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcggtggcg gatcgcccga tgtcaagtcg gcgacacgc
101 cgtcaaaacc ggccgcccc gttgttgctg aaaatgccgg ggaagggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcgcgag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaa atgccgccga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaacctgccc cctgcgaatg gcggtagcga ttttgaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaaataaac
501 gttgaccac tgtaaaggcg attcttgtaa tgggtgataa ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaagcgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaaacc acctactcgt tctgcacggt cgaggaggtc gttccggcc
751 gagattccgc tgattcccg caatcaggcc gatacgtga ttgtggatg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttg
951 cacggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatgaaa cggctttaag gggacttga
1151 cggaaaatgg cggcgggat gtttcggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

g287. pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```

		10	20	30	40	49
m287.pep		MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----				KETEA
		:	:	:	:	:
g287		MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA				
		10	20	30	40	50
		50	60	70	80	90
m287.pep		KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDAEVAQNMPQNAAGT				109
		:	::			
g287		AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNMPQNAA--				
		70	80	90	100	110
		110	120	130	140	150
m287.pep		DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDPSAGGQNAGNTA				169
g287		-----				
		170	180	190	200	210
m287.pep		AQGANAQAGNNQAAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGFSQNITLTHCKGDS				229
		: : : :			: : :	: : :
g287		-ESANQTGNNQFAGSSDSAPASNPAPANGGSDFGRTNVGNSVVIDGFSQNITLTHCKGDS				
		120	130	140	150	160
		230	240	250	260	270
m287.pep		CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP				289
		: : : :		: :	: :	: :
g287		CNGDNLLEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVRKKDGTNKYIIFYTD				
		180	190	200	210	220
		290	300	310	320	330
m287.pep		KPTSFAFRFRSARSRRSLPAEMPLIPVNOADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT				349
		:		:		
g287		KPPT-----RSARSRRSLPAEIPVNOADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT				
		240	250	260	270	280
		350	360	370	380	390
m287.pep		YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS				409
				: :		
g287		YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS				
		300	310	320	330	340
		410	420	430	440	450
m287.pep		KSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYR				469
g287		KSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYR				
		360	370	380	390	400
		470	480	489		
m287.pep		PTDAEKGFGVFAKGKEQDX				

g287 PTDAEKGGFGVFAGKKDRDX
420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

```

a287.seq
1    ATGTTTAAAC  GCAGTGTGAT  TGCAATGGCT  TGTATTGTTG  CCCTTTCAGC
51   CTGTGGGGGC  GCGGTGGCG  GATCGCCCGA  TGTTAAGTCG  CGCGACAGCG
101  TGTCAAAACC  TGCCGCCCT  GTTGTACTG  AAGATGTCGG  GGAAGAGGTG
151  CTGCCGAAAG  AAAAGAAAGA  TGAGGAGGCG  GTGAGTGGTG  CGCCGCAAGC
201  CGATACGCAG  GACGCACCG  CCGGAAAAGG  CGGTCAAGAT  ATGGCGGCAG
251  TTTCCGCGCA  AAATACAGGC  AATGGCGGTG  CGGCAACAAC  GGATAATCCC
301  GAAATAAAG  ACGAGGACG  GCAAAATGAT  ATGCCGCAAA  ATGCCGCCGA
351  TACAGATAGT  TCGACACCGA  ATCACACCCC  TGCACCGAAT  ATGCCAACCA
401  GAGATATGGG  AAACCAAGCA  CCGGATGCCG  GGAATCGGC  ACAACCGGCA
451  AACCAACGG  ATATGCCAA  TGCGCGCGAG  GGAATGCAGG  GGGACGATCC
501  GTCGGCAGG  GAAATGCCG  GCAATACGGC  AGATCAAGCT  GCAAAATCAAG
551  CTGAAACAA  TCAAGTCGG  GGCTCTCAAA  ATCTGCCTC  TTCAACCAAT
601  CCTAACGCCA  CGAATGGCG  CAGCGATTTT  GGAAGGATAA  ATGTAGCTAA
651  TGGCATCAAG  CTTGACAGCG  GTTCGGAATA  TGTAACGTTG  ACACATTGTA
701  AAGACAAAGT  ATGCGATAGA  GATTTCCTAG  ATGAAGAAGC  ACCACAAAAA
751  TCAGAATTG  AAAAATTAG  TGATGAAGAA  AAAATTAAAT  AAGATAAAAA
801  AGACGAGCAA  CGAGAGAATT  TTGTCGGTTT  GTTGCTGAC  AGGTAGAAAA
851  AGAATGGAAC  TAACAAATAT  GTCATCATTT  ATAAAGACAA  GTCCGCTTCA
901  TCTTCATCTG  CGCGATTACG  GCGTCTCGCA  CGGTTCGAGG  GGTTCGCTTC
951  GGCCGAGATG  CCGTGATTG  CCGTCAATCA  GCGCGGATAC  CTGATTGTCT
1001 ATGGGGAAGC  GGTCAGCCG  ACGGGGCATT  CGCGCAATAT  TCTCGCGCCC
1051 GAAGGGAATT  ACCGGTATCT  GACTTACGGG  GCGGAAAAAT  TGTCCGGCGG
1101 ATCGTATGCC  CTCAGTGTGC  AAGGCGAACC  GGCAAAAGGC  GAAATGCTTG
1151 CGGCGACCGG  CGTGTAACA  GGCGAAGTGC  TGCATTTCAC  TATGGA AAAA
1201 GGCCGTCCGT  CCCCCTCCG  AGCAGGTTT  CGCGAAAAG  TCGATTTCGG
1251 CAGCAAATCT  GTGGACGGCA  TTATCGACAG  CGCGATGAT  TTGCATATGG
1301 GTACGCAAAA  ATTCAAAGCC  GTTATCGATG  GAAACGGCTT  TAAGGGGACT
1351 TGGACGGAAA  ATGGCGCGCG  GGATGTTTTT  GGAAGGTTTT  ACGGCCCGGC
1401 CGGCGAAGAA  GTGGCGGGAA  AATACAGTCA  TCGCCCGACA  GATGCGGAAA
1451 AGGGCGGATT  CGGCCTGTTT  CCGCGCAAAA  AAGAGCAGGA  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep

1	<u>MFKRSVIAMA</u>	<u>CIVALSACGG</u>	GGGGSPDVKS	ADTLSPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDNP
101	ENKDEGPQND	MPQNAADTS	STPNHTPAPN	MPTRDMGNQA	PDAGESAQPA
151	NQPDMANAAD	GMQGDPTSAG	ENAGNTADQA	ANQAEENNQVG	GSQNPASSTN
201	PNATNGGSDF	GRINVANGIK	LDSGSENVTL	THCKDKVCDR	DFLDEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSARFRSA	RSRRSLPAEM	PLIPVNOADT	LIVDGEAVSL	TGHSGNIFAP
351	EGNYRYLTYG	AEKLSGGSYA	LSVQGEPAGK	EMLAGTAVYN	GEVLHFHMK
401	GRPSPSGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMGTQKFKA	VIDNGNFKGT
451	WTENGGGDVS	GRFYGPAGEE	VAGKYSRPT	DAEKGGFVGF	AGKKEOD*

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

[illegible]

m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDPSAGGQNAGNTA						
a287	: : : : : : : :						
	120	130	140	150	160	170	
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGVRDLANGVLIDGPSQNTLTHCKGDS						
a287	: : : : : : : : :						
	180	190	200	210	220	230	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGNDFVGLVADSVQMKGINQYIIIFYKP						
a287	: : : : : : : : :						
	240	250	260	270	280	290	
m287.pep	290	300	310	320	330	340	
	KP--TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
a287	:						
	300	310	320	330	340	350	
m287.pep	350	360	370	380	390	400	
	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYTRGRFAAKVDF						
a287	: :						
	360	370	380	390	400	410	
m287.pep	410	420	430	440	450	460	
	GSKSVDDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS						
a287							
	420	430	440	450	460	470	
m287.pep	470	480	489				
	YRPTDAEKGFGVFAGKKEQDX						
a287							
	480	490					

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA

```

```

701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAC
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGCG GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTG LTSLSTLNA PALSRTQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

```

              10      20      30      40      50      60
g406.pep    MRARLLIPILFSVFILSACGLTGTIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR
              |:|||||
m406        MQARLLIPILFSVFILSACGLTGTIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR

```

	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQGSGLTGGRYSIDALIRGEYINSPAVRTDITYPRYETTAETTSGGLTG					
m406	KVALYIATMGDQGSGLTGGRYSIDALIRGEYINSPAVRTDITYPRYETTAETTSGGLTG					
	130	140	150	160	170	180
g406 . pep	LTTSLSLTLNAPALSRTQSDGSGSRSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSLTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	190	200	210	220	230	240
g406 . pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAYKENYALWMGPYKVS KG I K P T E G L M V D F S D I Q P Y G N H T G N S A P S V E A D N					
m406	IKPKTNAFEAAYKENYALWMGPYKVS KG I K P T E G L M V D F S D I R P Y G N H T G N S A P S V E A D N					
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406 . seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCTC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406 . pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFQVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQGSGLTGG RYSIDALIRG EYINSPAVRT
101 DITYPRYETT AETTSGLTGT LTTSLSLTLN PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA

```

251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGQP *

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVDMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVDMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m406.pep	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGQPX					
a406	SHEGYGYSDEAVRRHRQGQPX					
	310	320				

EXAMPLE 2

Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 3

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 4

Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 5

Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

Immunol 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 8

Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

Table 2

225 gene variability: List of used *Neisseria* strains

Identification Strains number	Source / reference
Group B	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
Group A	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 Z2491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

Others

zo26_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998
 zo27_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998
 zo28_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998
 zo29_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

Gonococcus

zo32_225 Ng F62 R. Moxon / Maiden *et al.*, 1998
 zo33_225 Ng SN4 R. Moxon

fa1090 FA1090 R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z2491 <SEQ ID 3116>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRVPARRAGNA
 DELIGNAMGLNEQVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z001_225 <SEQ ID 3117>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Z002_225 <SEQ ID 3118>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Z003_225 <SEQ ID 3119>

MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Z004_225 <SEQ ID 3120>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z005_225 <SEQ ID 3121>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z006_225 <SEQ ID 3122>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z007_225 <SEQ ID 3123>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z008_225 <SEQ ID 3124>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z009_225 <SEQ ID 3125>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z010_225 <SEQ ID 3126>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z011_225 <SEQ ID 3127>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRFI
HAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z012_225 <SEQ ID 3128>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z013_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z014_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z015_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z016_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z017_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z018_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z019_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z020_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPINRAPARRAGNADELIGSAMGLNEQPVLPVNRVPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z021_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z022_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z023_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z024_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z025_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z026_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z027_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z028_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z029_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z032_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PVNRAPARRAG
NADELIGSAMGLNEQPVL PVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHI FKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z033_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVL PVNRAPARRAG
NADELIGSAMGLNEQPVL PVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHI FKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z096_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
Group B	
gnmzq01 NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02 BZ198	Seiler <i>et al.</i> , 1996
gnmzq03 NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04 1000	Seiler <i>et al.</i> , 1996
gnmzq05 1000	Seiler <i>et al.</i> , 1996
gnmzq07 BZ169	Seiler <i>et al.</i> , 1996
gnmzq08 528	Seiler <i>et al.</i> , 1996
gnmzq09 NGP165	Seiler <i>et al.</i> , 1996
gnmzq10 BZ133	Seiler <i>et al.</i> , 1996
gnmzq11 NGE31	Seiler <i>et al.</i> , 1996
gnmzq13 NGE28	Seiler <i>et al.</i> , 1996
gnmzq14 NGH38	Seiler <i>et al.</i> , 1996
gnmzq15 SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16 NGH15	Seiler <i>et al.</i> , 1996
gnmzq17 NGH36	Seiler <i>et al.</i> , 1996
gnmzq18 BZ232	Seiler <i>et al.</i> , 1996
gnmzq19 BZ83	Seiler <i>et al.</i> , 1996
gnmzq21 MC58	Virji <i>et al.</i> , 1992
Group A	
gnmzq22 205900	Our collection

gnmzq23	F6124	Our collection
z2491	Z2491	Maiden <i>et al.</i> , 1998

Group C

gnmzq24	90/18311	Our collection
gnmzq25	93/4286	Our collection

Others

gnmzq26	A22	(group W) Maiden <i>et al.</i> , 1998
gnmzq27	E26	(group X) Maiden <i>et al.</i> , 1998
gnmzq28	860800	(group Y) Maiden <i>et al.</i> , 1998
gnmzq29	E32	(group Z) Maiden <i>et al.</i> , 1998
gnmzq31	<i>N. lactamica</i>	Our collection

Gonococcus

gnmzq32	Ng F62	Maiden <i>et al.</i> , 1998
gnmzq33	Ng SN4	Our collection

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ01 <SEQ ID 3150>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANNT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ02 <SEQ ID 3151>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ03 <SEQ ID 3152>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ28 <SEQ ID 3173>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ29 <SEQ ID 3174>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ31 <SEQ ID 3175>
 MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGTS
 YQILDSVTTVSARARLVDSRNGKVLWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK*

GNMZQ32 <SEQ ID 3176>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ33 <SEQ ID 3177>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

Z2491 <SEQ ID 3178>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
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Group B

287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992

Group A

z2491	Z2491	Maiden <i>et al.</i> , 1998
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Gonococcus

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287_14 <SEQ ID 3179>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRNTVGNVVIDGPSQNTLTHCKGDS CSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYII FYKPKPTS FAR
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKKFKAIDGNGFKGTWTENGGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_2 <SEQ ID 3180>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNNGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRNTVGNVVIDGPSQNTLTHCKGDS CSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYII FYKPKPTS FAR
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKKFKAIDGNGFKGTWTENGGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_21. <SEQ ID 3181>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG
 QGAPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP
 NMLAGNMENQATDAGESSQPANQPDMAADGMQGGDDPSAGGQNAAGNTAAQGANQAGNNQ
 AAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNTLTHCKGDS CSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYII FYKPKPTS FARFRRS

ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD
DLHMGTOQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

287_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPVVTEDVGEEVLPKEKKDEEA
VSGAPQADTQDATAGKGGQDMAAVSAENTGNNGGAATTNPNKDEGPQNDMPQNAADTDS
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAANAADGMQGGDPSAGENAGNTADQA
ANQAEENQVGGSQNPASSTNPNATNGGSDFGRIINVANGIKLDSGSENVTLTHCKDKVCDR
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKDKSAS
SSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYG
AEKLSGGSYALSQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS
VDGIIDSGDDLHMGTOQKFAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT
DAEKGFGVFAGKKEQD*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA
AGGAPQADTQDATAGEGSDMAAVSAENTGNNGGAATTNPNKNEDEGAQNDMPQNAAESAN
QTGNQNPAGSSDSAPASNPAPANGGSDFGRTNVGNSVVIDGPSQNTLTHCKGDSNGDN
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNKYIIFYTDKPPTR
SARSRRSLPAEIPVQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGS
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGSKSVVDGIIDSG
DDLHMGTOQKFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGFG
VFAGKKDRD*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDEVAQNDMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMAANAADGMQGGDPSAGGQNAAGNTAAQGANQAGNNQ
AAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNTLTHCKGDSGSGNNFLDEEV
QLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMGKINQYIIFYKPKPSTSFARFRRS
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD
DLHMGTOQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

Group A

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Others

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

Gonococcus

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.

Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090_519 <SEQ ID 3185>
 MEFFIILLAAVAVFGFKSFVVIQQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
 LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
 ISAGMKIIDSSKTAK*

Z2491_519 <SEQ ID 3186>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV01_519 <SEQ ID 3187>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV02_519 <SEQ ID 3188>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV03_519 <SEQ ID 3189>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV04_519 <SEQ ID 3190>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV05_519 <SEQ ID 3191>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV06_519ASS <SEQ ID 3192>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV07_519 <SEQ ID 3193>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV11_519 <SEQ ID 3194>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV12_519 <SEQ ID 3195>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV18_519 <SEQ ID 3196>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV19_519 <SEQ ID 3197>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV20_519ASS <SEQ ID 3198>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
ISAGMKIIDSSKTAK*

ZV21_519ASS <SEQ ID 3199>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV22_519ASS <SEQ ID 3200>

MEFFIILLAAVVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV26_519 <SEQ ID 3201>

MEFFIILLAAVVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV27_519 <SEQ ID 3202>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV28_519 <SEQ ID 3203>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV29_519ASS <SEQ ID 3204>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREPEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSNKTAK*

ZV32_519 <SEQ ID 3205>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV96_519 <SEQ ID 3206>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Gr up B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

Group A

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Group C

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

Others

zm26	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

Gonococcus

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon

fa1090	FA1090	R. Moxon
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>
MKKHLRLSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
YFTPWQVAGNGSLAGTGTGYYEPVLKGDGRTERARFPIYGIPTDDFISVPLPAGLRSGKN
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELASGNEGVPVGALGTPLMGEYAGA
IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

Z2491 <SEQ ID 3208>
MKKYLFRALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM01 <SEQ ID 3209>
MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELASNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM02 <SEQ ID 3210>
MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
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QKTTGYVWQLLPNGMKPEYRP*

ZM03 <SEQ ID 3211>
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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELASNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
 LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
 LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
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 QKTTGYVWQLLPNGMKPEYRP*

ZM07 <SEQ ID 3215>

MKKYLFRAALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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 QKTTGYVWQLLPNGMKPEYRP*

ZM08N <SEQ ID 3216>

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 YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
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 QKTTGYVWQLLPNGMKPEYRP*

ZM09 <SEQ ID 3217>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
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 VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
 LVRIQRTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM11ASBC <SEQ ID 3219>
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YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM12 <SEQ ID 3220>
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM13 <SEQ ID 3221>
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YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM14 <SEQ ID 3222>
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YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
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KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM15 <SEQ ID 3223>
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM16 <SEQ ID 3224>
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LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKRFEGRFLPYHTRNQINGGAL
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KLQGTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM17 <SEQ ID 3225>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM19 <SEQ ID 3227>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM20 <SEQ ID 3228>

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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM22 <SEQ ID 3230>

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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQTGKNSGTIDNAGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL

KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM24 <SEQ ID 3232>

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YFTPWQVAGNGSLAGTVTGYEYVPLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYVPLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM26 <SEQ ID 3234>

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YFTPWQVAGNGSLAGTVTGYEYVPLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM27BC <SEQ ID 3235>

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YFTPWQVAGNGSLAGTVTGYEYVPLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
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ZM28 <SEQ ID 3236>

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YFTPWQVAGNGSLAGTVTGYEYVPLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATHPITR KALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM31ASBC <SEQ ID 3238>

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 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGRSFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM32ASBC <SEQ ID 3239>

MKKHLLRSALYGIAAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKA
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGRSFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGGDPVGALGTPLMGGYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM33ASBC <SEQ ID 3240>

MKKHLLRSALYGIAAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGRSFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGRSFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF	primer	Sequence	Restriction sites
001	Forward	CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGTCTTGTCAC	XhoI
003	Forward	CGCGGATCCCATATG-GTCGTATTCGTGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATCATGAACACGCGC	XhoI
005	Forward	CGCGGATCCCATATG-GACAATATTGACATGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCACATCCGCCCCG	XhoI
006	Forward	CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGTTCCGGCTTTGATGT	XhoI
007	Forward	CGCGGATCCCATATG-GCCGACAACAGCATCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGGCGTTCATGATATAAG	XhoI
008	Forward	CGCGGATCCCATATG-AACAACAGACATTTTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward	CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCTTTTGCCACGTTTT	XhoI
011	Forward	CGCGGATCCCATATG-AAGACACACCGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGGTCAGTACGGT	XhoI
012	Forward	CGCGGATCCCATATG-CTCGCCCGTTGCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward	CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGATTCGGCAAAAAATCT	XhoI
018	Forward	CGCGGATCCCATATG-CAGCAGAGGCAGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGAGGCGAACGCC	XhoI
019	Forward	AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	Eco RI
	Reverse	AAACTGCAG-TCAGCGGGCGGGGACAATGCCCAT	Pst I
023	Forward	AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse	AAACTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward	AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse	AAACTGCAG-TCAGAACGCGATATAGCTGTTCGG	Pst I
031	Forward	CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATGTAAGACGGGGACAAC	XhoI
032	Forward	CGCGGATCCCATATG-CGGCGAAACGTGC	BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGACTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTAAGTCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGCGAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAAACCTTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTCACCTCCGCCGC	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG-TTAATCCTGCAACACGAATTCGCCCCGTCCG	Pst I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	BamHI-
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward	CGCGGATCCCATATG-GTCATCATAACAGGCG	XhoI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	XhoI
	Reverse	AAACTGCAG-TCAAGATTCGACGGGGATGATGCC	Eco RI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Pst I
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	Eco RI
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	Pst I
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	BamHI-
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGCGGAGGAAAC	NdeI
	Reverse	AAAAAAGTCGAC-TCAGGCGGCGTTTTTCACCTTCCT	XhoI
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCCAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGTCTGCCAGTTTCAG	XhoI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGGAAGTCAACACCCATTATCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAAACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTTT	Pst I
111	Forward	CGCGGATCCCATATG-TGTTCGGAACAAACCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAA	XhoI
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTGAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	XhoI
122	Forward	CGCGGATCCCATATG-GTCATGATTAAAATCCGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATTT	XhoI
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGCACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
			XhoI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Pst I
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Pst I
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA	XhoI
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCCTTCAAAACCTTAATTTG	Eco RI
	Reverse	AAAAAACTGCAG-TCACCATGTCTGGCATTGAAAAAC	Pst I
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	XhoI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	XhoI
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCCAATTCGATCC	Kpn I
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	Pst I
137a	Forward	AAAAAAGAATTC-GGCCGCAAACACGGCATCGGCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Pst I
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTTCATG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	XhoI
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Pst I
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Eco RI
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Xba I
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAAACTGGG	Pst I
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTTGGAAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Xba I
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTTGGAACACGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Xba I
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	BamHI-

	Reverse	CCCGCTCGAG-AAACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	XhoI
151	Forward	AAAAAAGAATTC- ATGAAACAAATCCGCAACATCGCCATCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC- ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCCGACGAAATACTCAGACTTTTCGG	Pst I
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTTCCAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTTGCCCGCCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTTCGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAAACGGGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTTGCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTTCCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	BamHI-
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	NdeI
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	XhoI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCCG	BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NdeI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	EcoRI-
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	NdeI
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	XhoI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	BamHI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTTG	XhoI
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	BamHI-
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	NdeI
	Reverse	CCCGCTCGAG-CGACTTGGTTACCGCG	HindIII
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	BamHI-
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	NdeI
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	XhoI
248	Forward	CGCGGATCCCATATG-CGCAAACAGAACACT	BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	BamHI-
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	NdeI
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	XhoI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	NdeI
			XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	NheI
			XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCCTG	BamHI-
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	NdeI
			XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	NdeI
			XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	NdeI
			XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	NdeI
			XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGGG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTTCGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	NdeI
			XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	XhoI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCATCACGATGATGCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Pst I
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	XhoI
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAACCAG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	Pst I
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Pst I
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	XhoI
284	Forward	CGCGGATCCCATATG-TTGCCTGCAAAAGAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAAGT	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTCCGAAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	EcoRI- NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	XhoI
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
			BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTGATTTTTGCGGATGATTT	XhoI
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	Pst I
295	Forward	CGCGGATCCCATATG-AACCGGCCGGCCTCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	XhoI
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	Pst I
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Pst I
299	Forward	CGCGGATCCGCTAGC-CTACCTGTCGCCTCCG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	XhoI
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	Pst I
305	Forward	AAAAAAGGTACC-GAATTTTTACCGATTTCAGCACCGGA	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCCCAACTTATCCAGCCTGACAG	Pst I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Kpn I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Pst I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	XhoI
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	XhoI
311	Forward	AAAAAAGGTACC-ATGTTCAAGTTTTGGCTGGGTGTTT	Kpn I
	Reverse	AAACTGCAG-ATGTTTCATATTCCTTCGCTTCGGC	Pst I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Kpn I
	Reverse	AAACTGCAG-TCAGTTTTTCATCGATTGAACCGG	Pst I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Pst I
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	XhoI
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTTCATTTACCCTTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Xba I
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Xba I
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTCACCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTGCGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTTCACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTCAAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTTCG	Eco RI
	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530	Forward	CGCGGATCCCATATG-AGTGCGAGCGCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531	Forward	AAAAAAGAATTC-TATGCCGCCGCCTACCAAATCTACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACACAGCGCCGTGCCGACGACAAG	Pst I
532	Forward	AAAAAAGAATTC-ATGAGCGGTCAGTTGGGCAAAGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
532a	Forward	AAAAAAGAATTC-TTGGGTGTCGCGTTTGAGCCGGAAGT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
535	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539	Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
	Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a	Forward	AAAAAAGAATTC-GGCAAAACTCGTCATGAATTTGC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a	Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAAACTTCCAAGTACTTGC	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547	Forward	AAAGAATTC-ATGTTCTGTAGATAACGGATTTAATAAAAC	Eco RI
	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548	Forward	AAAGAATTC-GCCTGCAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCC GCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTTGGGAATATGCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTTCATTTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTTCATTTCCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCCG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTCGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTGGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
			XhoI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Pst I
589	Forward	AAAAAAGAATTC- ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI- NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI- NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI- NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI- NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCTGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTTGTGTTTTAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGC GTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTCTGGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	Eco RI
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCCC	Pst I
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Eco RI
645	Forward	AAAAAAGAATTC-GTGGAACAGAGCAACACGTAAATCG	Pst I
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Eco RI
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Pst I
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Eco RI
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Pst I
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Eco RI
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Pst I
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Eco RI
650	Forward	AAAAAAGAATTC-ATGTCCAACTCAAACCATCGC	Pst I
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Kpn I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Pst I
	Reverse	AAAAAACTGCAG-TTATTTGCCAGTTGGTAGAATGCGGC	Eco RI
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGTAATTTTCATCGG	Pst I
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Eco RI
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Pst I
	Reverse	AAAAAACTGCAG-CTACGATTTCCGGCGATTTCACATCGT	Eco RI
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Pst I
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	BamHI- NdeI XhoI
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	Eco RI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	Pst I
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	BamHI- NdeI XhoI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTCCGCCGTCGGGC	Eco RI
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	Pst I
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	BamHI- NdeI XhoI
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	Eco RI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	Pst I
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTTGCCGACGATTTT	Eco RI
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Eco RI
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Pst I
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAAAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	XhoI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTTGGATACTTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	XhoI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Pst I
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	XhoI
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	Eco RI
	Reverse	AAAAAACTGCAG- TTAGTTTTGCCGGATAATATGGCGGGTGCG	Pst I
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	BamHI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	XhoI
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	XhoI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGGTTTTCGGTCAG	XhoI
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	XhoI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	XhoI
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	XhoI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	XhoI
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTGTCGGTTTGGGTATC	HindIII
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	XhoI
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	EcoRI- NdeI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGCTTGCCCTCCTTTAC	XhoI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	XhoI
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	XhoI
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	XhoI
743	Forward	CGCGGATCCCATATG-GACGGTGTGTGCCTGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	XhoI
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTTGCCCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	NdeI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	XhoI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	BamHI-
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTAA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTCTGTACAGCAGGGG	NdeI
768	Forward	CGCGGATCCCATATG-GCCCCGAAAAACCCG	XhoI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	BamHI-
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTGAGATTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	NdeI
772	Forward	CGCGGATCCCATATG-TTGCGGCGTTGGTGG	XhoI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	BamHI-
774	Forward	CGCGGATCCCATATG-TCCGTTTCACCCGTTCC	NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-GGCGTTGTTCGGATTTCG	XhoI
900	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward	CGCGGATCCCATATG-CCCGATTTTTCGATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward	CCGGAATTCTACATATG-TTGCACCTTCAAAGGATAATC	EcoRI- NdeI
	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward	AAAAAAGGTACC-ATGATGCAGCACAAATCGTTTC	Kpn I
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse	AAACTGCAG-TTAATATGGTTTTGTCTGTTTCG	Pst I
909	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGGTTTTGAAACTTTGGTTTT	XhoI
910	Forward	AAAGAATTC-GCATTGCGCGGCGACTCTGCCGAGCG	Eco RI
	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward	AAAGAATTC-GCTTTCGCGTGGCCGGCGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward	AAAAAAGAATTC- CAAATCCGTCAAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTCGC	Pst I
913	Forward	CGCGGATCCCATATG-GAAACCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward	AAAGAATTC-GACAGAATCGGCGATTGGAAGCACG	Eco RI
	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
2	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTC	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAACCGCCAATCCGCCGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTCGGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	NdeI
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	XhoI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	BamHI-
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
			XhoI
			BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
			BamHI-
			NdeI
	Reverse	GCCCAAGCTT-GGGTCGTTTGTTCGTC	HindIII
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	XhoI
972	Forward	AAAAAAGAATTC- TTGACTAACAGGGGGGGGAGCGAAATTAAAAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Xba I
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAAACGAAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Pst I
982	Forward	CGCGGATCCCATATG-GCAGCAAAAGACGTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	XhoI
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	XhoI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	BamHI-
			NdeI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	HindIII
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	EcoRI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	XhoI
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	BamHI-
	2		NheI
	Reverse	CCCGCTCGAG-AAACAGCCATTTGAGCGA	XhoI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	XhoI
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
			NheI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```
g001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG GTGTCGGCGA ACGAGGTGTC
 51  CGGCAGGGCT TCGCCCCGA TGGTGCTGGT CATCTGCCAG ACGCTGCCGA
101  AACGCGATAC TTTAAACGGC TCGGGTACGC ATACTTTACC GGTTTGGGCG
151  ATTTTGCCGA GGTCTGTGCG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCGGTTT GTAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301  CCGTCTGAAG CGATGTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCGGCTTCAT CGGGCAGGTG GGACAATACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```
g001.pep
  1  MLPOGKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGHTLTPVWA
 51  ILPRSLRSKS TIITFSARFF GSVCNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```
m001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CGGcAssCTT ss.GCTTGGA yGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTTAAACGGT TCGGGTACGC ATACTGTGCC GGTTTGGGCG
151  ATTTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCCTCCGCAT CGGGCAGGTG GGACAAGACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```
m001.pep
  1  MLPOGKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGHTVVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```
a001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CGGCAAGGCT TGGGCTTGGA TGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTTAAACGGT TCGGGTACGC ATACTGTGCC GGTTTGGGCG
151  ATTTTGCCGA GGTCTGTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCTTGTGCAT CGGGCAGGTG GGACAAAACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```
a001.pep
  1  MLPOGKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGHTVVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PASGRWDKT A*
```

m001/a001 96.2% identity over a 131 aa overlap

```

              10      20      30      40      50      60
m001.pep  MLPOGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGHTVVPVWAILPRSLRSKS
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a001.pep  MLPOGKAARRMSANEVCGKAWAWMVLVICQTLPKRDTLNGSGHTVVPVWAILPRSLRSKS
```

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m001.pep		MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
		:					
g001		MLPQGKAARRVSANEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRSKS					
		10	20	30	40	50	60
		70	80	90	100	110	120
m001.pep		TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
		:					
g001		TIITFSARFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
		70	80	90	100	110	120
		130					
m001.pep		PSASGRWDKTAX					
		: :					
g001		PASSGRWDNTAX					
		130					

1	ATGGTCGTAT	TCGTGGCTGA	AGGCGTATTC	GGTCGCGCTG	TTTTGGGTCA
51	CTTGGTATTG	CTCTTCGGTC	AGGGTGC GTT	TGAGTTCCGC	GTCAC TCGGT
101	TTTTTATACG	TGCGCGCGTC	GAGCCTTTG	CCTTCCGGTG	CGGCTTTGGT
151	TTTGCCCGCG	AGCGATTCGT	CGGCTTTGCG	GATGTCGATG	TGGCAGTAGC
201	CGTTGGGGTT	TTTAATCAGG	TAGTCTGTAT	GGTATTCCTC	GGCGTCGTAG
251	AAGTTTTTCA	GCGGTTCTGT	TTCAACAACG	AGGGGCAGTT	GGTATTTTTG
301	CTGCTCCGCT	TTGAGGGCGC	CGGCGATGAC	CGCTTTTTTC	CGCGGGTCTG
351	TGTAGTACAC	GCCGCTGCGG	TATTGCGTGC	GGCTGTCTGT	ACCATGTTTG
401	TTGAGGCTGG	TCGGATCAAC	GACGCGGAAA	TAATATTGCA	GGATGTCGTC
451	CAGgCTGagt	TTGTCTGGCAT	CGTaggtcac	tTTGACGGTC	TCGGCATGAC
501	CGTATGGCG	GTaggacact	tctTCgtanc	TcGGGtTTTC	CGTgttGCCG
551	TTGGCgttac	cGGATACCGC	gtcaACCACG	CCGTcgatgc	g ttggaAATa
601	ggCTTCCAAg	ccccaaaagc	agccgccggc	gaagtaaatg	gtgcccggtg
651	tcatgtattGC	TGa			

1 MVVFVAEGVF GRAVLGHLVL LFGQGAFEFG VTRFFIRCRV EAFALRCGFG
51 FARQRFVGFA DVDVAVAVGV FNQVVLMVFL GVVEVFQRFV FNNEGQLVFL
101 LLAFEGGGDD GFFGGVGVVH AA~~AV~~LAGVV TLFVEAGRIN DAEIILQDVV

151 QAEFVGIVGH FDGLGMTRMA VGHFFVRVFR VAVGVTGYRV NHAVDAL EIG
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTGCGCTG TTTTGGGTAA
51 CTTGgTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCAC TCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTGCGGGG CGGTCTTGGT
151 TTTGCCCGGC AGCGGTTCTG CAGCkTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGk CGGCGATGAC GGCTTTTTTCG kCGGGGTCGG
351 TG TAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTGCGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGGC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGCG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAAATA
601 GGCTTCCAAG CCCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221
1 MVVFVAEGIF GRAVLGNLXL LFGQGAFFEG VTRFFIRCRV EAFALRGGLG
51 FARQRFVSXA DVDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGXGDD GFFXGVGVVH AA AVLRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E I
201 GFQAPEAAXG EVNGARVHDF *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTGCGCTG TTTTGGGTAA
51 CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCAC TCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTGCGGTG CGGTCTTGGT
151 TTTGCCCGGC AGCGGTTCTG CCGCTTTGCG GATATCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTTCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTTCG GCGGGGTCGG
351 TG TAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTGCGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGGC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGCG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAAATA
601 GGCTTCCAAG CCCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep
1 MVVFVAEGIF GRAVLGNLVL LFGQGAFFEG VTRFFIRCRV EAFALRCGLG
51 FARQRFVGFA DIDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGGGDD GFFGGGVGVH AA AVLRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E I
201 GFQAPEAAAAG EVDGARVHDF *

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXL LFGQGAFFEGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVL LFGQGAFFEGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDALFQAEPAAXGEVDGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRGGLGFARQRFVXSXA					
g003	MVVFVAEGVFGRAVLGHLVLLFGQGAFFGVTRFFIRCRVEAFALRCGFGFARQRFVGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGVVEVFQRFVFNQQLVFLLLAFEGGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVVTLFVEAGRINDAEEILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
g003	RVAVGVAGYRVNHAVDALFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

1	ATGgtagAAC	GGCATATCCA	GCATTTCGGG	AACGGTCATC	TTCATTTGAT
51	GCGCCCATGC	CAACAagtgga	gccaaAatgtT	CGGCGGCAGG	GCCTacgatT
101	TCCGCGCCGA	TAAagcgggc	gGTGgctTTT	tcgGCataca	ggcgcaTatg
151	gCCTTTGTTT	ACCAGcatca	cgcggctgcg	accttgaTTT	TTGAACGATA
201	CTTCGCCgat	GACAAATTTCG	TCGGCTTGGT	ATTGCGCGGC	AACCTGCGCG
251	TATTTCAAAC	CGACAAAGCC	GATTTCGcga	ctggttaaACA	CCACGCCAAT
301	GGTgctgcgg	cGCAAACCGC	TGCCGATAtt	cgGtagcgg	ccccgcgtta
351	ttgcccggca	atcttacctt	ggtcggcggc	ttcatGCAGC	AGGGGCagtt
401	ggttggacgc	gtcgcccgca	ataAAGATAT	GCGGAATgct	ggtCTGCATg
451	gtCAGCGGAT	CGGCAACGGG	tacgccgcgc	gcgtctttgT	CGATATTGAT
501	GTTTTCCAAA	CCGATATtgT	CAACGTTCGG	ACGGCGACCT	ACGGCTGCCA

```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTCGCCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCG ATGATTCCGC CCAAACCGAA AATTTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

g004.pep

```

1 MVERHIQHLR NGHLLHMRPC QQVSQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHAAAA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAAQTAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTPR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMPM MIPPKPKIST
251 FTKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

m004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTCGCCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TAGTTTCAGAC CGACAAAGCC GATTTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTT TAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATTCGCCCA AACCGAAAT TTCAACTTTC
751 ACGCCCAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

m004.pep

```

1 MVERHIQHLR NGHLLMCPS QQVRQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVHQHAAAA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAD
101 GAAPQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPA KICGILVCMV
151 SGSATGTPRA SFSILIFSKP ILSTFGRRPT AASIYSATNT PFSPPSCSQW
201 STLPSASSLT SVLASRCSFN SSPNTAFASS ETTGSEMPM IPPPKKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

a004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCGG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTCGCCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCGGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCGTC GAGTTTGCC TCAGTTT TAG CATCCAAATG
651 CAGTTTCAAT TCTTACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATGCCACCCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

```

a004 . pep
  1  MVERHIQHLR  NGLHLMCP  SQQVRQMF  GGR  TYDFCADE  AA  GGFFGIQ  AHM
 51  AFVYQHHA  AA  ALVFERY  FAD  DKFVGLV  LRG  NLRVFQ  TDKA  DLRTGE  HYAD
101  GAAQA  TAADI  RVAAAL  SPAI  LPWSA  ASC  SR  GSWLD  ASPAI  KICGIL  VCIV
151  SGSAT  GTPRA  SFSIL  MFSKP  ILSTF  GRRPT  AASIY  SATNT  PFSP  SC  SQWT
201  STLPS  ASSLA  SVLASK  CSFN  SSPNT  AF  ASS  ETTG  SEM  PPM  MPPK  PKISTF
251  TPKRCNA*

```

m004/a004 94.9% identity over a 257 aa overlap

```

              10      20      30      40      50      60
m004 . pep    MVERHIQHLRNGHLHLMCP  SQQVRQMF  GGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
              |||||
a004          MVERHIQHLRNGHLHLMCP  SQQVRQMF  GGRTYDFCADEAAGGFFGIQAHMAFVYQHHA
              10      20      30      40      50      60

              70      80      90      100     110     120
m004 . pep    ALVFERYFADDKFVGLVLRGNLRVFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI
              |||||
a004          ALVFERYFADDKFVGLVLRGNLRVFQTDKADLRTGEHYADGAAQTAADIRVAAALSPAI
              70      80      90      100     110     120

              130     140     150     160     170     180
m004 . pep    LPWSAASC  SRG  SWLDAS  PAMKIC  GILVCM  VSGSAT  GTPRAS  FSILIF  SKPIL  STFG  RRP
              |||||
a004          LPWSAASC  SRG  SWLDAS  PAIKIC  GILVC  IVSGSAT  GTPRAS  FSILMF  SKPIL  STFG  RRP
              130     140     150     160     170     180

              190     200     210     220     230     240
m004 . pep    AASIYSATNTPFSPSCSQWTSTLPSASSLT  SVLASRCSFNSSPNTAFASSETTGSEMPPM
              |||||
a004          AASIYSATNTPFSPSCSQWTSTLPSASSL  ASVLASKCSFNSSPNTAFASSETTGSEMPPM
              190     200     210     220     230     240

              250
m004 . pep    IPPKPKISTFTPKRCNAX
              :|||
a004          MPPKPKISTFTPKRCNAX
              250

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

```

              10      20      30      40      50      60
m004 . pep    MVERHIQHLRNGHLHLMCP  SQQVRQMF  GGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
              |||||
g004          MVERHIQHLRNGHLHLMR  PCQQV  SQMF  GGRAYDFRADKAAGGFFGIQAHMAFVYQHHA
              10      20      30      40      50      60

              70      80      90      100     110     119
m004 . pep    ALVFERYFADDKFVGLVLRGNLRVFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA
              :|||
g004          TLIFERYFADDKFVGLVLRGNLRVFQTDKADLRTGKHHANGAAAQTAADIRVAAPRYCPA
              70      80      90      100     110     120

              120     130     140     150     160     170     179
m004 . pep    ILPWSAASC  SRG  SWLDAS  PAMKIC  GILVCM  VSGSAT  GTPRAS  FSILIF  SKPIL  STFG  RRP

```



```

|||||
g004      ILPWSAASCSRGSWLDASPAIKICGMLVCMVSGSATGTPRASLSILMFSKPILSTFGRRP
              130      140      150      160      170      180

180      190      200      210      220      230      239
m004.pep  TAASIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
|||||
g004      TAANIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
              190      200      210      220      230      240

240      250
m004.pep  MIPPKPKISTFTPKRCNAX
|||||
g004      MIPPKPKISTFTPKRCNA
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 19>:

```

g005.seq
1  ATGGGGATGG ACAATATTGA TATGTTTCATG CCTGAACAAG AGGAAATCCA
51  ATCAATGTGG AAAGAAATTT TACTGAATTA CGGTATTTTC CTGCTCGAAC
101 TGCTTACCGT GTTCGGCGCA ATTGCGCTGA TTGTGTTGGC TATCGTACAG
151 AGTAAGAAAC AGTCGGAAG CGGCAGTGTC GTACTGACAG ATTTTTCGGA
201 AAATTATAAA AAACAGCGGC AATCGTTTGA AACATTCTTT TTAAGCGAGG
251 AAGAGACAAA ACATCAGGAA AAAAAAGAAA AGAAAAAGGA AAAGCGGAA
301 GCCAAAGCAG AGAAAAAGCG TTTGAAGGAG GCGGGGAGA AATCTGCCGA
351 AACGCAAAAA TCCCGCCTTT TTGTGTTGGA TTTTGACGGC GATTGTATG
401 CACACGCCGT AGAATCCTTG CGTCATGAGA TTACGCGCGT GCTTTTGATT
451 GCCAAGCCTG AAGATGAGGT TCTGCTCAGA TTGGAAAGTC CGGGCGGCGT
501 GGTTACCGGT TACGGTTTGG CGGCTTCGCA GCTTAGGCGT TTGCGCGAAC
551 GCAATATTCC GCTGAccgtc gccgTCGATA AGGTCGCGGC AAGCGgccgc
601 tatatgatgg cgtgtgtgGC GGATAAAATT GTTTCGCTc cgtttgccgt
651 catcggttcg gtgggtgtgg tgGcggaagt gccGAATATC CaccgCctGT
701 TGAAAAACA TGATATTGAT GTGGATGTA TGACGCGCGG CGAATTTAAG
751 CGCACGGTTA CTTTTATGGG TGAAATACG GAAAAGGGCA AACAGAAATT
801 CCGGCAGGAA CTGGAGGAAA CGCATCAGTT GTTCAAGCAG TTTGTCAGTG
851 AAAACCGCCC CGGGTTGGAT ATTGAAAAAA TAGCGACGGG CGAGCATTGG
901 TTCGGCCGGC AGGCGTTGGC GTTGAACCTG ATTGACGAGA TTTCGACCAG
951 TGATGATTG TTTGTTGAAAG CGTTTGAAAA CAAACAGGtt aTCCAAGTGA
1001 AATATCAGGA GAAGCGAAGC CTGATCCAGC GCATTGGTTT GCAGGCGGAA
1051 GCTTCCGTTG AAAAGTTGTT TGCCAAACTT GTCAACCGGC GAGCGGATGT
1101 GATGTAG

```

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

```

g005.pep
1  MGMNDNIDFM PEQEEIQSMW KEILLNYGIF LLELLTVFGA IALIVLAIQV
51  SKKQSESGSV VLTDfSENYK KQRQSFETFF LSEETHKHQE KKEKKKEKAE
101 AKAEKKRLKE GGEKSAETQK SRLFVLDFDG DLYAHAVESL RHEITAVLLI
151 AKPEDEVLLR LESPggVVHG YGLAASQLRR LRERNIPLTV AVDKVAASGG
201 YMMACVADKI VSAPFAVIGS VGVVAEVPNI HRLLKKHDID VDVMtAGEFK
251 RTVTFMGENT EKGKQKFRQE LEETHQLFKQ FVSENRPGLD IEKIATGEHW
301 FGRQALALNL IDEISTSDDL LLKAFENKQV IEVKYQEKRS LIQRIGLQAE
351 ASVEKLFACL VNRRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 21>:

```

m005.seq
1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGGAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AwAGCGGCAG TGTCGTACTG ACGGATTTT CGGAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CACAACATCA GAAAAAGAG GAAAAGAAAA AGGAAAAGGC GGAAGCCAAA

```

```

301 GCAGAGAAAA A.CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATTCCGACA
801 GGAACGTGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQXSGSVVL TDFSENYKKQ RQSFEEFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS
351 VEKLFKLVN RRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTGCTACTG ACGGATTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GGAAGAGAG GAAAGAAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCCGC CTTTTGTGT TGGATTTTGA CGGCGATTG TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGAA AGTCCGGGCG GCGTGTTTCA
501 CGGTTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTGCGC GAACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGTTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATTCCGACA
801 GGAACGTGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEEFFLS GEEAKHQEKE EKKKEKAEAK
101 AEKKRLKEGG EKSETQKSR LFVLDFDGDY YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTVAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
 351 VEKLFKLVN RRADVM*

m005/a005 79.2% identity over a 366 aa overlap

	10	20	30	40	50	60
m005.pep	MDNIDMFMPQE	EIQSMWKEILL	NYGIFLLELLT	VFGAIALIVL	AIQSKQSXS	SGSVVL
a005	MDNIDMFMPQE	EIQSMWKEILL	NYGIFLLELLT	VFGAIALIVL	AIQSKQSE	SGSVVL
	10	20	30	40	50	60
	70	80	90	100	110	120
m005.pep	TDFSENYKKQR	QSFEAFFLSG	EAAHQEKEE	KKKEKAEAK	AEKXRLKEG	GEKSAETXKSR
a005	TDFSENYKKQR	QSFEAFFLSG	EAAHQEKEE	KKKEKAEAK	AEKXRLKEG	GEKSSSETQKSR
	70	80	90	100	110	120
	130	140	150	160	170	180
m005.pep	LFVLXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX
		:				
a005	LFVLDFDGDLY	AHAVESLRHEI	TAVLLIAKPE	DEVLLRLESP	GGVVHGYGLA	ASQLRRLR
	130	140	150	160	170	180
	190	200	210	220	230	240
m005.pep	XXXXXXXXXXXX	ASGGYMMACV	ADKIASAPFA	IVGSVGVVA	EVVNIHRLK	KHDIDVD
	:					
a005	ERNIPLTVAV	DKVAASGGY	MMACVADKIV	SAPFAIVGS	VGVVAEVVNI	HRLKHDIDVD
	190	200	210	220	230	240
	250	260	270	280	290	300
m005.pep	VMTAGEFKRTV	TFMGENTEK	GKQKFRQEL	EETHQLFKQ	FVSENRPQL	DIEEVATGEHWFG
a005	VMTAGEFKRTV	TFMGENTEK	GKQKFRQEL	EETHQLFKQ	FVSENRPQL	DIEEVATGEHWFG
	250	260	270	280	290	300
	310	320	330	340	350	360
m005.pep	RQALALNLID	EISTSDDLL	LKAFENKQV	IEVKYQEKQ	SLIQRIGLQ	AEASVEKLFKLVN
a005	RQALALNLID	EISTSDDLL	LKAFENKQV	IEVKYQEKQ	SLIQRIGLQ	AEASVEKLFKLVN
	310	320	330	340	350	360
m005.pep	RRADVMX					
a005	RRADVMX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

	10	20	30	40	50
m005.pep	MDNIDMFMPQE	EIQSMWKEILL	NYGIFLLELLT	VFGAIALIVL	AIQSKQSXS
g005	MGMDNIDMFMPQE	EIQSMWKEILL	NYGIFLLELLT	VFGAIALIVL	AIQSKQSE
	10	20	30	40	50
	60	70	80	90	100
m005.pep	VLTDSENYKKQR	QSFEAFFLSG	EAAHQEKEE	KKKEKAEAK	AEKXRLKEG
g005	VLTDSENYKKQR	QSFEAFFLSG	EAAHQEKEE	KKKEKAEAK	AEKXRLKEG
	70	80	90	100	110
	120				

	120	130	140	150	160	170
m005.pep	SRLFVLXX					
		:				
g005	SRLFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPPGGVVHGYGLAASQLRR					
		130	140	150	160	170
		180	190	200	210	220
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVAEVPNIHRLKKHDID					
	:	: : :				
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
		190	200	210	220	230
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTEKKGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHW					
	: : : : :					
g005	VDVMTAGEFKRTVTFMGENTEKKGKQKFRQELEETHQLFKQFVSENRPGLDIEKIATGEHW					
		250	260	270	280	290
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFACL					
	: : : : :					
g005	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKRSLIQRIGLQAEASVEKLFACL					
		310	320	330	340	350
	360					
m005.pep	VNRRADVMX					
g005	VNRRADVMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

g006.seq

```

1  ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCG CCTGAACAAC AGCTTGAAC gcgACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCGTCGGCG
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAA
301 GGCTACGGCA GCGCGGGGCA TATTTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGACG ATGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAA
451 GCCGGAACCT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

g006.pep

```

1  MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRVL ISNREAFGYL CVGAAMGILF GFAFVMTLK
101 GYGSAGHIYS VGTYLWMFAM SLDDVPRLVE QYSNLKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

m006.seq

```

1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCGTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCG CCTGAACAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACC GCGGCAGCT GTACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCGTCGGCA
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAA
301 GGCTACAGCA GCGCGGGGCA TGCTTATTCG GTCGGCACTT ATCTGTGGAT

```

```

351  GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401  ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451  GCCGGAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

```

m006.pep
  1  MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSLKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

```

a006.seq
  1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGC GTTGT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCG CCTGAAGAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GGACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCA
251 CCGCGATGGG TATTTTGCTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAACTT GA

```

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

```

a006.pep
  1  MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
51  KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSLKDIGQ RIEWSKRNIK
151 AGT*

```

m006/a006 96.7% identity over a 153 aa overlap

m006.pep	10	20	30	40	50	60
	MLLVLEFWVGVS AVGILALFLWLLPRFAAI SENLYFRLNNSLERDNHFIRKGDRRQLYRH					
a006	MLLVLEFWVGVS AVGILALFLWLLPRFAAI SENLYFRLKNSLERDNHFIRKGDERQLDRH					
	10	20	30	40	50	60
m006.pep	70	80	90	100	110	120
	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
m006.pep	130	140	150			
	SLDDVPRLVEQYSLKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSLKDIGQRIEWSKRNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

```

m006.pep
  1  MLLVLEFWVGVS AVGILALFLWLLPRFAAI SENLYFRLNNSLERDNHFIRKGDRRQLYRH

```

g006-1.seq

1	ATGTGGA AAA	TGTTGAAACA	CATAGCCAAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACATTT	TCCCCGGTCG	GACTGGAAAA	CCTTTTGATG	CTGGGGTATC
101	CGGTGTTTGG	CGGCTGGGCG	ATTAATGCCG	TGATTGCGGG	GAGGGTGTGG
151	CAGGCGTTGC	TGTACGCTTT	GGTGTATTT	TTGATGTGGC	TGGTCGGTGC
201	GGCACGGCGG	ATTGCCGATA	CGCGCACGTT	TACGCGGATT	TATACCGAAA
251	TCGCCGTGCC	GGTTGTGTTG	GAACAACGGC	AGCGGCAAGT	CCCGCATTTCA
301	GCGGTAAC TG	CACGGGTTGC	CCTGTCGCGT	GAATTTGTCA	GCTTTTTTGA
351	AGAACACCTG	CCGATGTCCG	CGACATCCGT	CGTATCCATA	TTCGGCGCTG
401	GCAATCATGT	GCTGGTGCCT	GAATTTTGGG	TCGGCGGTGC	GGCGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTGCCG	CCATCAGCGA
501	AAACCTGTAT	TTCCGCCTGA	ACAACAGCTT	GGAACGCGAC	AACCACTTTA
551	TCCGAAAAGC	CGACGAGCGG	CAGCTGTACC	GCCATTACGG	ACTGGTTTCG
601	CGCCTGCGTG	TGCTGATTTT	C AACCGCGAA	GCCTTCGGGT	ATCTCTGCGT
651	CGGCGCGGCG	ATGGGTATTT	TGTTCCGGCT	TGCTTTTGTG	ATGATGACGC
701	TCAAAGGCTA	CGGCAGCGCG	GGGCATATTT	ATTGCGTTCG	CACTTATCTG
751	TGGATGTTTT	CCATGAGTTT	GGACGATGTG	CCGCGATTGG	TCGAACAATA
801	TTCCAATTTG	AAAGACATCG	GACAACGGAT	AGAGTGGTCG	GAACGGAACA
851	TCAAAGCCGG	AACTTGA			

g006-1.pep

1	MWKMLKHIAK	THRKRLLIGTF	SPVGLENLLM	LGYPVFGGWA	INAVIAGRNV
51	<u>QALLYALVVF</u>	<u>LMWLVGAAARR</u>	IADTRTFTRI	YTEIAVPVVL	EQRQRQVPHS
101	AVTARVALSR	EFVSFFEEHL	PIAATSVVSI	<u>FGACIMLLVL</u>	EFWVGVSavg
151	<u>ILALFLWLLP</u>	RFAAISENLY	FRLNNSLERD	NHFIRKGDGR	QLYRHYGLVS
201	RLRVLISNR	AFGYLCVGAA	MGILFGFAFV	MMTLKGYGSA	GHIYSVGTYL
251	WRFAMSLDDV	PRLVEQYSNL	KDIGORIEWS	ERNIKAGT*	

```
m006-1.seq
1  ATGTGGAAAA  TGTGAAACA  CATAGCCCAA  ACCCACC GCA  AGCGATTGAT
51  TGGCACATTT  TCCCTGGTCG  ATCATGGAAA  CCTTTTGATG  CTGGTGTATC
101 CGGTGTTTGG  CGGCCGGGCG  ATCAATGCCG  TGATTGCGGG  GGAGGTGTGG
151 CAGGCGTTGC  TGTACGCTTT  GGTGTGCTT  TTGATGTGGC  TGGTGGTGC
201 GGTGCGGCGG  ATTGCCGATA  CGCGCACGTT  TACGCGGATT  TATACCGAAA
251 TCGCCGTGCC  GGTGCTGTTG  GAACAGCGGC  AGCGACAAGT  CCCGATTTCG
301 GCGGTAAC TG  CGCGGGTTGC  CCTGTCGCGT  GAGTTTGTC A  GCTTTTTTGA
351 AGAACACCTG  CCGATTGCCG  CGACATCCGT  CGTATCCATA  TTCGGCGCGT
401 GCATCATGCT  GCTGGTGCTG  GAATTTTGGG  TCGGCGTGTC  GCGCGTGGGC
451 ATACTTGCGT  TGTTTTTATG  GCTTTTGCCA  CGTTTTGCCG  CCATCAGCGA
501 AAACCTGTAT  TTCCGCGCTG  ACAACAGCTT  GGAACCGCAG  AACCACTTTA
551 TCCGAAAAGG  CGACCGGCGG  CAGCTGTACC  GCCATTACCG  ACTGCTTGCG
601 CGCCTGCGTG  TGCTGATTTT  CAACCGCGAA  GCCTTCGGCT  ATCTCTGCGC
```

```

651 CGGCACGGCG ATGGGTATTT TGTTCCGGCTT TGCTTTTGTG ATGATGACGC
701 TCAAAGGCTA CAGCAGCGCG GGGCATGTCT ATTCGGTCGG CACTTATCTG
751 TGGATGTTTG CCATGAGTTT GGACGACGTG CCGCGATTGG TCGAACAATA
801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
851 TCAAAGCCGG AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 34; ORF 006-1>:

```

m006-1.pep
  1 MWKMLKHIAQ THRKRLIGTF SLVGLENLLM LVYPVFGGRA INAVIAGEVW
 51 QALLYALVVL LMWLVGAVRR IADTRTFTRI YTEIAVPVVL EQRQRQVPHS
101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGVSavg
151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGD RR QLYRHYGLLA
201 RLRVLISNRE AFGYLCVGTa MGILFGFAFV MMTLKGYSSA GHVYSVGTYL
251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

```

m006-1/g006-1 95.5% identity in 288 aa overlap

m006-1.pep	10	20	30	40	50	60
	MWKMLKHIAQTHRKRLIGTFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL					
g006-1	10	20	30	40	50	60
	MWKMLKHIAKTHRKRLIGTFSPVGLENLLMLGYPVFGGWAINAVIAGRvwQALLYALVVF					
m006-1.pep	70	80	90	100	110	120
	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
g006-1	70	80	90	100	110	120
	LMWLVGAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
m006-1.pep	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVSavgILALFLWLLPRFAAISENLYFRLNNSLERD					
g006-1	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVSavgILALFLWLLPRFAAISENLYFRLNNSLERD					
m006-1.pep	190	200	210	220	230	240
	NHFIRKGD RR QLYRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA					
g006-1	190	200	210	220	230	240
	NHFIRKGD RR QLYRHYGLVSR LRVLISNREAFGYLCVGAAMGILFGFAFVMMTLKGYGSA					
m006-1.pep	250	260	270	280	289	
	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
g006-1	250	260	270	280		
	GHIYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

```

a006-1.seq (partial)
  1 ..AGCCAAAACC ACCGCAAGCG ATTGATTGGC ACATTTTTTC TGGTCGGACT
 51 GGAAAACCTT TTGATGCTGG TGTATCCGGT GTTTGGCGGC TGGGCGATTA
101 ATGCCGTGAT TGCGGGGCG GCGTGCGAGG CGTTGCTGTA CGCTTTGGTT
151 GTGCTTTTGA TGTGGCTGGT CCGTGCGGCG CGGCGGATTG CCGATACGCG
201 CACGTTTACG CGGATTATA CCGAAATCGC CGTGCCGGTT GTGTTGGAAC
251 AGCGGCAGCG GCAAGTCCG CATTGCGCGG TAACTGCGCG GGTGCCCCTG
301 TCGCGTGAGT TTGTCAGCTT TTTTGAAGAA CACCTGCCGA TTGCCGCGAC
351 ATCCGTCGTA TCCATATTCG GCGCGTGCAT CATGCTGCTG GTGCTGGAAT
401 TTTGGGTCGG CGTGTGCGCG GTGGGCATAC TTGCGTTGTT TTTATGGCTT
451 TTGCCACGTT TTGCCGCCAT CAGCGAAAAC CTGTATTTCG GCCTGAAGAA
501 CAGCTTGGAa CGCGACAACC ACTTTATCCG AAAAGGCGAC GAGCGGCAGC
551 TGGACCGCCA TTACGGACTG CTTGCGCGCC TCGGTGTGCT GATTTCCAAC
601 CGCGAAGCCT TCGGCTATCT CTGCGTCGGC ACGGCGATGG GTATTTTGTT
651 CGGCTTTGCT TTTGTGATGA TGACGCTCAA AGGCTACAGC AGCGCGGGGC

```

701 ATGTCTATTC GGTCGGCACT TATCTGTGGA TGTGTGCCAT AAGTTTGGAC
 751 GACGTGCCGC GATTGGTCGA ACAATATTCC AATTTGAAAG ACATCGGACA
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)

1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWVGVS VGILALFLWL
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN
 201 REAFGYLCVG TAMGILFGFA FVMMLTKGYS SAGHVYSVGT YLWMFAISLD
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT *

a006-1/m006-1 95.7% identity in 280 aa overlap

a006-1.pep	10	20	30	40	50
	SQNHRKRLIGTFFLVGLENLLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	10	20	30	40	50
	MWKMLKHIAQTHRKRLIGTFFSLVGLNLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
a006-1.pep	60	70	80	90	100
	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
m006-1	60	70	80	90	100
	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
a006-1.pep	120	130	140	150	160
	PIAATSVVSIFGACIMLLVLEFWVGVSAGVILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	120	130	140	150	160
	PIAATSVVSIFGACIMLLVLEFWVGVSAGVILALFLWLLPRFAAISENLYFRLNNSLERD				
a006-1.pep	180	190	200	210	220
	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLTKGYSSA				
m006-1	180	190	200	210	220
	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLTKGYSSA				
a006-1.pep	240	250	260	270	280
	GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX				
m006-1	240	250	260	270	280
	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq

1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTGTGCT GCCTCTGcgC
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa
 201 cgTCCTgctg cacagcatgg tcaaaggcAt cgacgggaca ttcaaagtgg
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep

1 MNTTRLPTAF ILCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
 51 TAFPPLFRSD CIMNKPHVLL HSMVKGIDGT FKVERQNLRR IYARNRHQRC
 101 GHCRRRHLYH ERL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

m007.pgp

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 41>:

a007.seq

This corresponds to the amino acid sequence <SEO ID 42; ORF 007.a>:

a007.pgp

m007/a007 97.3% identity over a 113 aa overlap

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

m007/g007

[illegible]

g007 CIMNKPHVLLHSMVKGIDGTFKVERQNLRRRIYARNRHQRCGHCRRRHLYHERL
 70 80 90 100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGGA AGGCGCGGCG
151 ACTGCGTTTC CTCCGCTTTT CCGGTCGGAC TATATTATGA ACAAACCGCA
201 CGTCCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCC CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAACA GGCAAAAGGC AAAAAAAC.
```

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)

```

1  MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
51  TAFPPLFRSD YIMNKPHVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAAACGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCC CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAACA GGCAAAAGC AAAAAAACT
401 AA
```

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep

```

1  MNTTRLPTAL VLGCFCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51  TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN*
```

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
g007-1	MNTTRLPTAFILCCLCAAAS	AADNSIMTKGQKVYESNCIACHGKKGEGRG	TAFPPLFRSD			
	10	20	30	40	50	60
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
g007-1	YIMNKPHVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
m007-1.pep	TEKDVQAKSKKNX					
g007-1	TEKDVQAKGKKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
```

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAAACA GGCAAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1 MNTTRLPTAL VLGCLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

```

              10      20      30      40      50      60
m007-1.pep  MNTTRLPTALVLGCFCAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD
              |||
a007-1      MNTTRLPTALVLGCLCAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD
              10      20      30      40      50      60

              70      80      90      100     110     120
m007-1.pep  FIMKKPQVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV
              |||
a007-1      FIMKKPQVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV
              70      80      90      100     110     120

              130
m007-1.pep  TEKDVQAKSKKNX
              |||
a007-1      TEKDVQAKNKK
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1 ATGAACAACA GACATTTTGC CGTCAtcgCC TTGGGCAGCA ACCTTGACAA
51 CCCGCACAA CAAATacgcg gcg cattaga cgcgctctcg tcccatcctg
101 acatccggct tgaaCagggt tcctcactgt aTatgaccgc acctgtcggt
151 tacgAcaaTC agcccgATTT CATCaatgcc gTCTgcaccg TTTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAAccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGCC TTACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAAATACG GAAAGGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1 MNNRHFVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTLDG IALLAELNRI EADFGRRERF RNAPRTL DLD
101 IIDFDGISSD DPRLTLEHPR AHERSEFVIRP LAEILPDFIL GKYGKVVELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT TGTCaATGCC GTCTGCACCG TTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAct CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACctTGCC

```

182

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTGTTTTA GGAAACACG GAAAGGTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRETSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHGKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis*<SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTG CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAT CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGAC TCACCTGCGC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATAACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAACACG GAAAGGTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRETSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFIL GKHGKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
	10	20	30	40	50	60
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

```

m008/g008
      10      20      30      40      50      60
m008.pep MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA
g008     MNNRHFAVIALGSNLDNPAQQIRGALDALSSHPDIRLEQVSSLYMTAPVGYNQPDFINA

```

183

	10	20	30	40	50	60
	70	80	90	100	110	120
m008 . pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
g008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008 . pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008	AHERSFVIRPLAEILPDFILGKYGKVVELSKRLGNQGIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009 . seq

1	ATGCCCCGCG	CTGCCGTAGC	CTTTGAGCGT	CATCATCACA	AAAGCAAAGC
51	CGAACAAAAT	ACCCATCGCC	GCGCCGACGC	AGAGATAGCC	GAAGGCTTCG
101	CGGTTGGAAA	TCAGCACACG	CAGGCGCGAA	ACCAGTCCGT	AATGGCGGTA
151	CAGCTGCCGC	TCGTGCCTT	TTCGGATAAA	GTGGTTGTcg	cGTTCCAAGC
201	TGTTGTTTTCAG	GCGGAAATAC	AGGTTTTCGC	TGATGGCGGC	AAAACGTGGC
251	AaaaGCCATA	A			

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009 . pep

1	MPRAAFAFER	HHHKSKEQN	THRRADAEIA	EGFAVGNQHT	QARNQSVMAV
51	QLPLVAFSDK	VVVAFAQVVQ	AEIQVFADGG	KTWQKP*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009 . seq

1	ATGCCCCGCG	CTGCTGTAGC	CTTTGAGCGT	CATCATCACA	AAAGCAAAGC
51	CGAACAAAAT	ACCCATCGCC	GTGCCGACGC	AGAGATAGCC	GAAGGCTTCG
101	CGGTTGGAAA	TCAGCACACG	CAGGCGCGCA	AGCAGTCCGT	AATGGCGGTA
151	CAGCTGCCGC	CGGTGCCTT	TTCGGATAAA	GTGGTTGTTCG	CGTTCGAAGC
201	TGTTGTTTTCAG	GCGGAAATAC	AGGTTTTCGC	TGATGGCGGC	AAAACGTGGC
251	AAAAGCCATA	A			

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009 . pep

1	MPRAAFAFER	HHHKSKEQN	THRRADAEIA	EGFAVGNQHT	QARKQSVMAV
51	QLPPVAFSDK	VVVAFAQVVQ	AEIQVFADGG	KTWQKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009 . pep	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009 . pep	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009	VVVAFAQVVQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
  1 ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
 51 CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTTCCTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
  1 MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
 51 QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVQAEIQVFADGGKTWQKPX					
	:					
a009	VVVAFAQVLQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
  1 ATGGGTTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
 51 TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTTGC TAAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCAGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTTCGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTGCT TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTGCGC CCGTGCGGGC ATTCGGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGGAG GCGGTATTC TGTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgctatgc GCcgACCGta aAagaCTTGG
851 CTTCTCGCga cgtGGTTTCA CgcgcGatgG CGatggaAat ctatgaaggt
901 cgcggtctgTG GtaaaAAcaA agaCCacgtC TTACTGAAAA TCGACcAtAt
951 cggtGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTCCA
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTcgc aCCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGSDDLWLG DQDAIEFMCR AAPEAVIELE
101 HMGMFPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDDVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCCKNKDHF LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

m010.seq (PARTIAL)

```

1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTGT CTAAAGTGT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GyCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCCGTGCCA
401 ATACGCAATT CTTTGTGGAA TGGACGGCAC AAGATTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACCGCCATG GAAATGGAAA CCGGCGAaT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGG CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGGCGTGG CGGGTGCGG CGTGTGATT ACCGAA...

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

m010.pep (PARTIAL)

```

1  ..XQLSKSGLNC AVLSKVFPTR SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSDWLGDQD AIEFMCRAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQQN VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMFQWQFQP TGAVAGAVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

a010.seq

```

1  ATGGGCTTTC CTGTTCCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGTATTTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCGCA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGCGT ACGGCGCGAG GCGGATATTC TGTTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCA CGTTGTTC CCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CCGGCGAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATTCG ACCAAGTACC ATGGCGAAGT
1101 TGTGTTTCTT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCCTGCTA

```

```

1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGA CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGACAGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGGCGACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATCA GATGCCAATA CCTTGTCCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
  1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
 51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101  HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151  QQNVRRANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201  ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251  VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301  RGCGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351  TTHYMMGGIP TNYHGEVVVP QGDEYEVVPK GLYAAGECAC ASVHGANRLG
401  TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451  DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMATA ERVKRTEIKD
501  KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551  NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                                XQLSKSGLNCAVLSKVF PTRSHTVAAQGGISASXGNV
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCAVLSKVF PTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
a010      QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENG DVVG V
a010      GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENG DVVG V
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

m010.pap/q010.pap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

1	ATGGGTTTTTC	CTGTTTCGCAA	GTTTGATGCC	GTGATTGTCTG	GCGGTGGCGG
51	TGCAGGTTTTA	CGTGCAGCCC	TCCAATTATC	CAAATCCGGT	TTGAATTGTG
101	CCGTTTTTGTC	TAAAGTGTCTC	CCGACCCCGT	CGCATACCGT	AGCGGCGCAG
151	GGCGGTATTT	CGCGCTCTCT	GGGTAATGTG	CAGGAGGACC	GTTGGGACTG
201	GCACATGTAC	GATACCGTGA	AAGGTTCCGA	CTGGCTGGGC	GACCAAGATG
251	CGATTGAGTT	TATGTGTCGC	GCTGCGCCTG	AAGCGGTGAT	TGAGTTGGAA
301	CACATGGGTA	TGCCTTTTGA	CCGCGTTGAA	AGCGGCAAAA	TTTATCAGCG
351	TCCTTTTCGGC	GGACATACTG	CCGAACATGG	TAAACGTGCG	GTAGAACCTG
401	CATGTGCGGT	TGCCACCGT	ACCGGTCATG	CGATTGTGCA	TACTTTGTAC
451	CAACAAAACG	TCCGTGCCAA	TACACAATTG	TTTTGTGGAAT	GACGCGCGCA
501	AGATTTGATT	CGTGATGAAA	ACGGCGATGT	CGTCGGCGTA	ACCGCCATGG
551	AAATCGGAAAC	GGGCGAAGTT	TATATTTTCC	ACGCCAAGGC	CGTGATGTTT
601	GCTACCGGTG	GCGGCGGTCT	TATTTATGCT	TCTTCTACCA	ATGCTTATAT
651	GAATACCGGT	GACGGTTTGG	GCATTTGCGC	CCGTGCGGGC	ATTCGGTTGG
701	AAGATATGGA	ATTCTGGCAA	TTCCACCCGA	CCGGCGTGGC	GGGTGCGGGC
751	GTGTTGATTA	CCGAAGGCGT	ACGCGGCGAG	GGCGGTATTC	TGTTGAACGC
801	CGACGGCGAA	CGCTTTATGG	AACGCTATGC	CCCGACCGTA	AAAGACTTGG
851	CTTCTCGCGA	CGTGGTTTCA	CGCGCGATGG	GCGTGGAAT	CTATGAAGGT
901	CGCGGCTGTG	GTAAAAACAA	AGACCACGTG	TTACTGAAAA	TCGACCATAT
951	CGGTGCAGAA	AAAATTATGG	AAAAACTGCC	GGGCATCCGC	GAGATTTCCA
1001	TTTCAGTTTGC	CGGTATCGAT	CCGATTAAAG	ACCCGATTCC	GGTTGTGCCG
1051	ACTACCCACT	ATATGATGGG	CGGCATTCCG	ACCAATTATC	ACGGTGGAAT
1101	TGTTGTTTCCG	CAAGGCGACG	AGTACGAAGT	ACCTGTAAAA	GGCCTGTATG
1151	CCGCAGGTGA	GTGCGCCTGT	GCTTCCGTAC	ACGGTGCGAA	CCGTTTGGGT

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPPFDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPIVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

g010-1 / P10444

sp|P10444|DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 191/303 (63%), Positives = 238/303 (78%)

```

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV 60
      M PVR+FDAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN
Sbjct: 1 MKLPVREFDAVVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG 120
      ED W+WHMYDTVKGSD++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
Sbjct: 61 HEDNWEWHMYDTVKGSDYIGDQDAIEYMCKTGPEAILELEHMG L PFSRLDDGRIYQRPFG 120

Query: 121 GHAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V 180
      G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL++++G VVG
Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNHTTIFSEWYALDLVKNQDGA VVGC 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
      TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ
Sbjct: 181 TALCIETGEVVYFKARATVLTGGAGRIYQSTTNAHINTGDGVGM AIRAGVPVQDMEMWQ 240

Query: 241 FHPTGVAGAGVVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300
      FHPTG+AGAGVL+TEG RGE GG LLN GERFMERYAP KDLA RDVV+R++ +EI EG
Sbjct: 241 FHPTGIAGAGVVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGR DVVARSIMIEIREG 300

Query: 301 RGC 303
      RGC
Sbjct: 301 RGC 303

```

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 53/102 (51%), Positives = 62/102 (60%)

```

Query: 309 HVLLKIDHIGAEKIMEKLP GIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
      H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
Sbjct: 310 HAKLKL D HLGKEVLESRLPGILELSRTFAHVD PVKEPIPV IPTCHYMMGGIPTKV T GQAL 369

Query: 369 VPQGDEYEV PVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
      +V V GL+A GE AC SVHGANRLG NSLLDLVVF
Sbjct: 370 TVNEKGEDVVVPGLFAVGEIACSVHGANRLGGNSLLDLVVF 411

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTC CTGTTCCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGTATATT CCGCTCTCTT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

```

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451 CAACAAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTCT TATTTATGCG TCTTCTACCA ATGCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GGCGGTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTCGTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCAGGTGA GTGACCCGCG CAACGTATCG AGCGTTTGGG CAACCAAACC
1351 GATGGTGAAA ACGTTGATGC ATTGCGTCCG GAAGTCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVFP TRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVPV QGEDYEVPVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFTDEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

	10	20	30	40	50	60
m010-1.pep	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGGISASLGNV					
g010-1	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGGISASLGNV					
	10	20	30	40	50	60
m010-1.pep	QEDRWDWHMYDTVKGSDWLGQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
g010-1	QEDRWDWHMYDTVKGSDWLGQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
m010-1.pep	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V					
g010-1	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V					
	130	140	150	160	170	180
m010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					
g010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240
m010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					
g010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					

190

	190	200	210	220	230	240
m010-1.pep	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
g010-1	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
m010-1.pep	310	320	330	340	350	360
	RGCGKNKDHVLLKIDHIGA EKIMEKLP GIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
g010-1	310	320	330	340	350	360
	RGCGKNKDHVLLKIDHIGA EKIMEKLP GIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
m010-1.pep	370	380	390	400	410	420
	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHGANRLGTNSLLDLVVFGKAAGDSMIK					
g010-1	370	380	390	400	410	420
	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHGANRLGTNSLLDLVVFRPTPRX					
m010-1.pep	430	440	450	460	470	480
	FIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQRSVQLHAGVFRTDEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCTG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGCGCT ACGGCGCGAG GCGGTATTTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATTCCG ACCAAGTACC ATGGCGAAGT
1101 TGTGCTTCCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGA CAATCAAAGT
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CTTGCTCCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MGFPVRKFDV VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGSDDLW DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPVPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKLPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFR TDEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / a010-1 99.3% identity in 587 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFD	AVIVGGGGAGL	RAXLQLSKSGLN	CAVLSKVFP	TRSHTVAAQGGIS	SASLGNV
a010-1	MGFPVRKFD	AVIVGGGGAGL	RAALQLSKSGLN	CAVLSKVFP	TRSHTVAAQGGIS	SASLGNV
	10	20	30	40	50	60
a010-1.pep	70	80	90	100	110	120
a010-1.pep	QEDRW	DWHMYDTV	KGSDWLG	QDAIEFMCRAA	PEAVIELEHM	GMPFDRVESGKIYQRPFG
m010-1	QEDRW	DWHMYDTV	KGSDWLG	QDAIEFMCRAA	PEAVIELEHM	GMPFDRVESGKIYQRPFG
	70	80	90	100	110	120
a010-1.pep	130	140	150	160	170	180
a010-1.pep	GHTAEHGKRA	VERACAVADRT	GHAMLHTLYQ	QNV RANTQFF	VWETAQDLIR	DENG DVVG V
m010-1	GHTAEHGKRA	VERACAVADRT	GHAMLHTLYQ	QNV RANTQFF	VWETAQDLIR	DENG DVVG V
	130	140	150	160	170	180
a010-1.pep	190	200	210	220	230	240
a010-1.pep	TAMEMETGEV	YIFHAKAVMF	FATGGGGRIY	ASSTNAYMNT	GDGLGICARAGI	PLEDMFWQ
m010-1	TAMEMETGEV	YIFHAKAVMF	FATGGGGRIY	ASSTNAYMNT	GDGLGICARAGI	PLEDMFWQ
	190	200	210	220	230	240
a010-1.pep	250	260	270	280	290	300
a010-1.pep	FHPTGVAGAG	VLITEGVRGE	GGILLNADGER	FMERYAPTVK	DLASRDVVSRA	MAMEIYEG
m010-1	FHPTGVAGAG	VLITEGVRGE	GGILLNADGER	FMERYAPTVK	DLASRDVVSRA	MAMEIYEG
	250	260	270	280	290	300
a010-1.pep	310	320	330	340	350	360
a010-1.pep	RGCGKNKDHV	LLKIDHIGAE	KIMEKLP GIR	EISIQFAGID	PIKDPVPVPT	THYMMGGIP
m010-1	RGCGKNKDHV	LLKIDHIGAE	KIMEKLP GIR	EISIQFAGID	PIKDPVPVPT	THYMMGGIP
	310	320	330	340	350	360
a010-1.pep	370	380	390	400	410	420
a010-1.pep	TNYHGEVVVP	QGDEYEV PVK	GLYAAGECAC	ASVHGANRLG	TNSLLDLVVF	GKAAGDSMIK
m010-1	TNYHGEVVVP	QGEDYEV PVK	GLYAAGECAC	ASVHGANRLG	TNSLLDLVVF	GKAAGDSMIK
	370	380	390	400	410	420
a010-1.pep	430	440	450	460	470	480
a010-1.pep	FIKEQSDWKLP	PANAGELTRQ	RIERLDNQT	DGENVDALRR	ELQRSVQLHAG	GVFR TDEILS
m010-1	FIKEQSDWKLP	PANAGELTRQ	RIERLDNQT	DGENVDALRR	ELQRSVQLHAG	GVFR TDEILS
	430	440	450	460	470	480
a010-1.pep	490	500	510	520	530	540
a010-1.pep	KGVREVMAIA	ERVKRTEIKD	KSKVWNTARI	EALELDNLIE	VAKATLVSAE	ARKESRGAHA
m010-1	KGVREVMAIA	ERVKRTEIKD	KSKVWNTARI	EALELDNLIE	VAKATLVSAE	ARKESRGAHA
	490	500	510	520	530	540
a010-1.pep	550	560	570	580		
a010-1.pep	SDDHPERDDE	NWMKHTLYHS	DANTLSYKPV	HTKPLSVEYI	KPAKRVYX	

m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVYX
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG
401 CCGTCGAAGC AGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGGATATG
451 GGCAAAGTGA TGGTCGTATT GAAAACccGC CTCGCCGGCA AAGccgATAT
501 GGGCGAAGTC AACAAAATCT TGAAAAccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG
401 AGGTCGAAGC TGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGGATATG
451 GGTAAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSA	VCFAFQTASK	PAVSIRHPSE	DIMSLKIRLT	EDMKTAMRAK	DQVSLGTIRL
g011	MKTHRKTCSA	VCFAFQTASK	PAVSIRHPSE	DIMSLKTRLT	EDMKTAMRAK	DQVSLGTIRL
	10	20	30	40	50	60
	70	80	90	100	110	120
m011.pep	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDSAKIY	TEAGRQDLADK	ENAEIEVLHR
g011	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDGAKIY	TEAGRQDLADK	ENAEIDVLHR

193

	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKTRLAGKA					
	:					
g011	YLPQMLSAGEIRTAVEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGEVNKILKTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

```

1   ATGCTCGCCC GTCGCTATTT TTTCAATATC CAACCCGGGG CGGTTTTTCAC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCGCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACa
201 gGcggTGGAT ATTCGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAAACAAT TTTATCCGCC acacacgcca tcatatagcc
301 gcCGCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GCAGATTTCT CCCC GCCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTTC CTGATGTTT GTCTCTTCTC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

```

1   MLARRYFFNI QPGAVFTDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRHFRHHTHR TDDRKRSGNN FIRHTRHHIA
101 AACRDLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFRGFLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFCLFLA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

```

1   ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCGCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnnnnnnnC AACACAAAAA GGCGTGATTT nTGC GTTTTCG
551 GCAGATTTCT CCCCACCCCTC CTTCAAACGT TTTTCcTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTGT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

```

1   MLARCHFLNI QLR AVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRHHTHR TDNRKRSGSN FIRHTRHHIT
101 AARXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXQHKKA*F XRFRGFLPTL LQTFFLCFGF
201 RLFLFLFLFF LMLCLFPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCCGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GAAGATTCTT CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m012.pep	NIMFFQQAVIDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAAARXXXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQAVIDIRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m012.pep	XXQHKKAXF					
a012	PKLRSRQTVTVNHAARTFQSKQNLIFRLGNQKHRRLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
m012.pep	XRFGRLPTLLQTFFLCFGRFLFLFLFLFFLMCLFPAX					
a012	LRFGRFLPTLLQTLFLCFGRFLFLFLFLFFLMFCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

195

	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXXX					
	: : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
	130	140	150	160	170	180
m012.pep	XXXQHKKAXF					
	:	:	:	:	:	
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	190	200	210	219		
m012.pep	XRFGRFLPTLLQTFFLCFGRFLFLFLFLFLMLCLFPAX					
	: : : : :					
g012	190	200	210			
	LRFGRFLPALQLTFLCFGRFLFLFLFLFLMFLCLFLAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGTTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CTTTTCCTGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGCGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGAG  CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCGGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CCGCGAAACG CyTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GCAGATTTCT CCCCACCTC  CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT  CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHHTR TDNRKSGSN FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT XKLSRQTVT  VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFLFLFA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	: : : : :					
g012	10	20	30	40	50	60
	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
	70	80	90	100	110	120
m012-1.pep	NIMFFQQAVDIRYFRHHHTRTDNRKSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	: : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
	130	140	150	160	170	180
m012-1.pep	XKLSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	: : : : :					
g012	PKLRSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180	
	190	200	210	219			
m012-1.pep	LRFG	RFLP	TLQL	TLFL	CFGR	FLFLFLFLMFC	LPAX
g012	LRFG	RFLP	ALLQ	TLFL	CFGR	FLFLFLFLMFC	LFLAX
	190	200	210				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTCCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTTCACCA
201 GCGCGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CCGCAAACG CTTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACACG
401 CGCCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGCCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GAAGATTCTC CCCACCCCTC CTTCAAACGC TTTTCTCTCT CTTTGCGCTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCFLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60	
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI						
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI						
	10	20	30	40	50	60	
	70	80	90	100	110	120	
a012-1.pep	NIMFFQQAVDIRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT						
m012-1	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT						
	70	80	90	100	110	120	
	130	140	150	160	170	180	
a012-1.pep	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF						
m012-1	XKLRSRQTVT VNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF						
	130	140	150	160	170	180	
	190	200	210	219			
a012-1.pep	LRFG	RFLP	TLQL	TLFL	CFGR	FLFLFLFLMFC	LPAX
m012-1	LRFG	RFLP	TLQL	TLFL	CFGR	FLFLFLFLMFC	LPAX
	190	200	210				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTtgt tcataataca
51  gtCcgaccGG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCTTTTCT
101 TGCCGTGGCA GGCGATGCag tTgGATTCTGT AACTTTTTTG CCCTTTtGtc

```

g013.pcp

m013.seq

m013.pgp

a013.seq

a013.pap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPRSPFLPWQATQLDSYTFPCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPRSPFLPWQATQLDSYTFPCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIVGSFMFETLLILRSGXKIFLPNQX					
	:					
a013	AQRQPKTRAVGSRVVFIVGSMLMFETLLILRSGXKIFLPNRX					
	70	80	90	100		

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

198

m013/g013

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	: : : : :					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNAVPRPSPFLPWQAMQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFVIGVSF-MFETLLLLILR-SGXKIFLPNQX					
	: : : : : : :					
g013	AQRQHKMKAVGSRVVFVIGVSPNVLKPCFLILPLRGEKFFWPKSGIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 93>:

g015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTTTTTTCCT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGT CGGCTTTTGG AAAGCACTGC CCCACCTCAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGCA CAAAAATCCT GCTCCTGTTC GCCTACATCG
251 CACTGGGCAT GGTAATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCTAT GTGTTGCATC GCCTGCATCG TTTACCTTGC
351 CAAAACCAAA GTCCTGCCAT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 94; ORF 015.ng>:

g015.pep

```

1  MQYLIVKYSH QIFVTITILV FNIRFFLLWK NPEKPLVGFV KALPHLNDTM
51  LLFTGLWLMK ITHFSPFNAP WLGTKILLLF AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 95>:

m015.seq (partial)

```

1  .AAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51  CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCCGTT CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC
151 GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC ACCGTTTACC TGCTCGCCAT GTGTTGCGTC GCCTGCATCG
251 TTTACCTTGC CAAAACCAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 96; ORF 015>:

m015.pep (partial)

```

1  .KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
51  AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 97>:

a015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTGTTTTCNT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAAACCAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 98; ORF 015.a>:

a015.pep

199

1 MQYLIVKYSH QIFVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY
 101 TVYLLAMCCL TCIVYLAKTK VLPF*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCLTCIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFFLLWKNPEKPLVGFVKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
g015	FSPFNAPWLGTKILLLLFAYIALGMVMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg
 101 tctttgTCGA TATTGATGTT TTCCAAACCG ATAtgtCAA CGTTCGGACG
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTCGC
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC
 251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT
 51 ATYGCQHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QQQFFSEHGF

101 RLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

```
m018.seq
1   ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51  GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCACG GCTGCCAGCA TATATTCCGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

```
m018.pep
1   MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51  AAHGCGHIFG NKYAFAILL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

```
a018.seq
1   ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCCGCAATA AAGATATGCG
51  GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCTACG GCTGCCAGCA TATATTCCGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGGCC
251 TCGGTTTTAG CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

```
a018.pep
1   MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51  AAYGCGHIFG NKYAFAILL PMDFYIAVCV EFGLGFSIQM QFQFFTEHGF
101 RLV*
```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	10	20	30	40	50	60
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVDFQTDIVNVRTAAYGCGHIFG					
	70	80	90	100		
m018.pep	NKYAFAILLPMDFYIAVCI EFDLGFSIQM QFQFFAEHGVRLVX					
	70	80	90	100		
a018	NKYAFAILLPMDFYIAVCV EFGLGFSIQM QFQFFTEHGFRLVX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

```
m018/g018
10 20 30 40 50 60
m018.pep MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG
||| |||||:| ::|||:|||||:| |||||:| |||:|||||:|||||:|||||
g018 MQQGQLVGRVARNKDMRNAGLHGQRVGNRYAARVFDIDVDFQTDIVNVRTATYGCQHIFG
10 20 30 40 50 60
```

201

	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX			
g018	NKYAFFAILLPMDFYIAVCVEFDLGFSIQMQFQFFSEHGFRVLX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

```

g019.seq (partial)
  1  ..ctgctggcgg ccctgggtgct tgccgcgtgt tcttcgACAA ACacactGCC
 51  AGCCGGCAAG ACCCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101  GCGTTCCAC cgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151  GGCGGCTACC CGTCCGCACT GGATGCAGTG AAACAGAACA ACGATGCGGC
201  AGCCGCCGCC TATTTGAAA Acgcaggaga cagCGcgatg gcGGAAAtg
251  tccgcaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

```

g019.pep (partial)
  1  ..LLAALVLAAC SSTNTLPAGK TPADNIETAD LSASVPTRPA EPEGKTLADY
 51  GGYPSALDAV KQNDAAAAA YLENAGDSAM AENVRKEWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

```

m019.seq (partial)
  1  ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
 51  GCTTGCCGCG TGTTCTTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101  CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151  CGCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201  ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251  AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301  AAGTCTTTGG GCGCACGCAG ACAGTGGACG CTGTTTGCAC AGGAATACGC
351  CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401  CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451  AAAGTGCCTT CGGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCCG
501  CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGC GCGGA CTGCTGGCCG
551  GCGCCCAAAC CACAGACGCA CGCAACCTTG CCGCCGATT GGGCAGCCCG
601  TTTGACGGCG GTACACAAGG TCGCGCGGAA TATGCCCTGT TGAACGTCAT
651  CGGCAAAGAA GCACGCAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701  TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751  GGGCATTATC AGTCGCAAAA CCTCAATGTG CTGCGCCCT TGGACTATTA
801  CGCAAGGTT GCGGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851  ACGCCCGCGC CGCCTTGCGC GCGGACGCTT GGGACGAGCT GGCCTCCGTT
901  ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951  GCTGGCACGC AGCCGCGCCG CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GCGGCAGCG ACGGGCAGGA ATTTTATGC GGTGCTGGCA
1051 GGGGAAGAAT TGGGTCGGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGCAAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAACGCG
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTGGC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTTG
1351 CGCTATATTT CGCGGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCTGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCGGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

```

m019.pep (partial)
  1  MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYGKV ADRRQLTDDQ IEWYARAALR ARRWDELASV
301 ISHMPEKLQK SPTWLYWLAR SRAATGNTQE AEKLYKQAAA TGRNFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQV SOSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNLYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

```

a019.seq
1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCTGGT
51  GCTTGCCGCG TGTTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCNCCCT
151 CCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCG
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCCG AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CCGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCCT TGGACTATTA
801 NGGCAGGTT GCCGACCGCC GCGCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCNCNTNNGC NNNCGNNGTT NGNANGANNNT GGCNCCGNN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCAGCG AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAAC
1001 TNTACAAACA GGCGGCAGCA NCGGGCANGA ATTTTATGCT NGTGCTGNCN
1051 GGGGAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCTCC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGGTGCT GTTCGAAAC AGCCGAACCG CCGCGATGC GAAATGCGC
1201 CGTCNGGCTC AGGCGGAATG GCGTTTCGCC ACACGCGGCT TCGATGAAGA
1251 CAAGCTGCTG ACCGCCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACCTCA CTACACCTTG
1351 CGTACATTT CGNNNNNTNA NGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTCGTCAG GAAAGCGCT
1451 TCGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCCGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCGCCTG CAAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCAG GGCGCGCCGA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCCT ACTACGCCTC CCTCTTCGGC
1801 CGCCCGCACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

```

a019.pep
1  MYPPSLKHSL PLLVLVLAA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAAXX XRXXXXXXAXX
301 XXXXXXXXXX XXXXXXXXAR SRAATGNTQX AXKLYKQAAA XGXFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFQV SRTAGDAKMR
401 RXAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNLYTL

```


203

451 RYISXXXTDV IRHAQNVNVD PAWVYGLIRQ ESRFVMAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADGNIRMGY WYMADTKRRL QNNEVLATAG
551 YNAGPGRARR WQADTPLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG
601 APHIPLKQRM GIVPAR*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLP	SMKHS	LPLLA	ALVLA	ACSS	TNTL
a019	MYPP	SLKHS	LPLLV	XLVLA	ACSS	TNTL
	10	20	30	40	50	60
m019.pep	70	80	90	100	110	120
	YGGY	PSAL	DAVK	QKND	AAVA	AYLE
a019	YGGY	PSAL	DAVK	QKND	AAVA	AYLE
	70	80	90	100	110	120
m019.pep	130	140	150	160	170	180
	PAGRA	QVECY	ADSS	RNDY	TRAA	ELVK
a019	PAXRA	QVECY	ADSS	RNDY	TRAA	ELVK
	130	140	150	160	170	180
m019.pep	190	200	210	220	230	240
	LLAGR	QTTDA	RNLAA	ALGSP	FDGG	TQGS
a019	LLAGR	QTTDA	RNLAA	ALGSP	FDGG	TQGS
	190	200	210	220	230	240
m019.pep	250	260	270	280	290	300
	EQRS	FAWGL	GHYQS	QNLNV	PAALD	YVGK
a019	EQRS	FAWGL	GHYQS	QNLNV	PAALD	YVGK
	250	260	270	280	290	300
m019.pep	310	320	330	340	350	360
	ISHM	PEKL	QKSPT	WLWLA	RSRA	ATGNT
a019	XXXX	XXXX	XXXX	XXXX	XXXX	XXXX
	310	320	330	340	350	360
m019.pep	370	380	390	400	410	420
	RNNV	PDAG	KNSVR	MAEDG	AVKRA	LVLF
a019	RNNV	PDAG	KNSVR	MAEDG	AVKRA	LVLF
	370	380	390	400	410	420
m019.pep	430	440	450	460	470	480
	TAAQ	TAFD	HGFY	DMAVN	SAERT	DRKLN
a019	TAAQ	TAFD	HGFY	DMAVN	SAERT	DRKLN
	430	440	450	460	470	480
m019.pep	490	500	510	520		
	ESRF	VIGA	QSRV	GAQGL	MQVMP	ATARE
a019	ESRF	VIGA	QSRV	GAQGL	MQVMP	ATARE
	490	500	510	520	530	540
a019	QNNE	VLAT	AGYN	AGPGR	ARRWQ	ADTP
	550	560	570	580	590	600

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAEPEGKTLAD				
m019	MYLPSMKHSLPLLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAEPEKTLAD					
		10	20	30	40	50
		50	60	70	80	89
g019.pep	YGGYPSALDAVKQNNDAAYLENAGDSAMAENVRKEWL					
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLFAQEYAKLE					
		70	80	90	100	110
						120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

1	ATGGTAGAAC	GTAAATTGAC	CGGTGCCCAT	TACGGTTTGC	GCGATTGGGT
51	AATGCAGCGT	GCGACTGCGG	TTATTATGTT	GATTTATACC	GTTGCACTTT
101	TAGTGGTTCT	ATTTGCCCTG	CCTAAAGAAT	ATCCGGCATG	GCAGGCATTT
151	TTTAGTCAAG	CTTGGGTAAA	AGTATTTACC	CAAGTGAGCT	TTATCGCCGT
201	ATTCTTGAC	GCTTGGGTGG	GTATCCGCGA	TTTGTGGATG	GACTATATCA
251	AACCCTTCGG	CGTGCCTTTG	TTTTTGCAGG	TTGCCACCAT	TGtctGGCTG
301	GTCCGCTGCC	TCGTGTATTC	AGTTAAAGTG	ATTTGGGGGT	AA

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

1	MVERKLTGAH	YGLRDWVMQR	ATAVIMLIYT	VALLVVLFA	PKEYPAWQAF
51	FSQAWVKVFT	QVSFIAVFLH	AWVGIRDLWM	DYIKPFGVRL	FLQVATIVWL
101	VGCLVYSVKV	IWG*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

1	ATGGTAGAAC	GTAAATTGAC	CGGTGCCCAT	TACGGTTTGC	GCGATTGGGT
51	GATGCAACGT	GCGACTGCGG	TTATTATGTT	GATTTATACC	GTTGCACTTT
101	TAGTGGTTCT	ATTTTCCCTG	CCTAAAGAAT	ATTCGGCATG	GCAGGCATTT
151	TTTAGTCAAA	CTTGGGTAAA	AGTATTTACC	CAAGTGAGCT	TCATCGCCGT
201	ATTCTTGAC	GCTTGGGTGG	GTATCCGCGA	TTTGTGGATG	GACTATATCA
251	AACCCTTCGG	CGTGCCTTTG	TTTTTGCAGG	TTGCCACCAT	CGTTTGGCTG
301	GTCCGCTGTC	TCGTGTATTC	AGTTAAAGTG	ATTTGGGGGT	AA

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

1	MVERKLTGAH	YGLRDWVMQR	ATAVIMLIYT	VALLVVLFS	PKEYSAWQAF
51	FSQTVWKVFT	QVSFIAVFLH	AWVGIRDLWM	DYIKPFGVRL	FLQVATIVWL
101	VGCLVYSVKV	IWG*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

1	ATGGTAGAAC	GTAAATTGAC	CGGTGCCCAT	TACGGTTTGC	GGGATTGGGC
51	GATGCAACGT	GCGACGCGG	TTATTATGTT	GATTTATACC	GTTGCACTTT
101	TAGTGGTTCT	ATTTGCTCTG	CCTAAAGAAT	ATTCGGCATG	GCAGGCATTT
151	TTTAGTCAAA	CTTGGGTAAA	AGTATTTACC	CAAGTGAGCT	TCATCGCCGT

205

201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA
 251 AACCTTCGG CGTGCGTTTG TTTTGCAGG TTGCCACCAT CGTCTGGCTG
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVL FAL PKEYSAWQAF
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPFVRL FLOVATIVWL
 101 VGCLVYSIKV IWG*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYTVALLVVLFALPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
a023	QVSFIAVFLHAWVGIRDLWMDYXKPFVRLFLQVATIVWLVGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFALPKEYPAWQAFFSQAWVKVFT					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq
 1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTcATT GCAGGCAATT
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgt ATGTGCCGCC
 201 CGTGCAAact gcgcccgttt ATTGCGCTCC TGCTTATGTT CCGCcgctCTG
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC
 301 aacgCGGCGa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTc
 351 caaAcgCtac CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
 401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCaggA
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC
 501 TGCCGCGCAA ACCCTGTGA AACCCGCCG gcaACCGCCC GTTCAGTCCG
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC
 601 GCGCCCGCCC CGCAATCTCC TGCCGCTTCG CCTTCCGGCA CGCGTTCGGT
 651 CGGCGGCATT GTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAAA TTGCTGGTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTCAGC AGGTGCTTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTC GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
1  MLKQTTLLAA CTAAVALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51  TPYNAAPAAAN DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFRW NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEGQQVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
1  ..GTGCCGCCG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTCC
51  GCCGTCTGCA CCTGCCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTCC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCACCG AAAGCCGCAG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTCC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCCTGTGAAA CCCGCCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TGCGGAAAAT AAAGCGGTTT CCGCGCCCGC
651 CCCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTCT GTCGGCGGCA
701 TTGTTTGGCA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCCGCGGC
751 AACAACAAGG GTGTCGATAT TGCCGTAAT GCGGGACAGC CCGTTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGGTCA
951 GCAGGTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGTGCG TCAAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
1  ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51  NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNMLSIGQIV KVKPAGYAAP KTAAVESRPA VPAAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRPT QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSGL RGYGNLVIIQ HNSSFLLTAYG
301 HNQKLLVGEG QQVKRGQOVA LMGNTDASRT QLHFEVRQNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
1  ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TTGCCGCTCA
51  GTTGGGCGGA TGCCCCACCC AACACCTTC TCCTGTCATT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

```

```

151  ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201  GGTGCAAAGC GCGCCGGTTT ATANGCCTCC TGCTTATGTT CCGCCGTCTG
251  CACCTGCCGT TTCGGGTACA TACGTTCCTT CTTACGCANC CGTCGACATC
301  AACGCGGCCG CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351  CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
401  CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA
451  TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501  TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCCG
551  CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601  CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651  GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701  CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751  ACCCCTGTGA AACCCGCCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801  TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCGCAAT
851  CTCCTGCCGC TTCGCCTTCC GGCACGCGTT CGGTGCGCGG CATTGTTTGG
901  CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951  GGGTGTGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTGT GCGGCGGCTG
1001 ACGGCAAAGT GGTTTATGCA GGTTCGGTT TGAGGGGATA CGGCAATTG
1051 GTCATCATCC AGCATAATTC TTCCTTCTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTCGAGGTG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

```

a025.pep
  1  MLTP TTL*VA CTALAAQLGG CPTQHPSPIV AGNSGMQTVP SAPVYNPYGA
 51  TPYNAA PAAN DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101  NAATH TIVRG DTVYKISKCY HISQDD FRAW NGMTDN TLSI GQIVKVKPAG
151  YAAPK AA AVK SRPAVP AAAQ PLVQSAP VDI NAATH TIVRG DTVYNISKRY
201  HISQDD FRAW NGMTDN TLSI GQIVKVKPAG YAAPK AA AVK SRPAVP AA VQ
251  TPVKP AA QPP VQSAPQ PAAP AAENKAV PAP APQSPA ASPS GTRSVGGIVW
301  QRPTQ GK VVA DFGGNN KGVD IAGNAGQ PV L AAADGKV VYA GSGLRGYGNL
351  VIIQH NS SFL TAYGHN QKLL VEGEQV KRG QQVALMG NTE ASRTQLHFEV
401  RQNGK FVNPN SYIAF*

```

m025/a025 97.4% identity over a 351 aa overlap

```

                                10      20      30
m025.pep                                VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                |||:|||||
a025      GMQTVPSAPVYNPYGATPYNAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
              40      50      60      70      80      90

              40      50      60      70      80      90
m025.pep      YAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMTDN TLSIGQIVKVKPAGYAAP
              || |||:|||||
a025      YAXVDINAATH TIVRGDTVYKISKCYHISQDD FRAWNGMTDN TLSIGQIVKVKPAGYAAP
              100     110     120     130     140     150

              100     110     120     130     140     150
m025.pep      KAAAVKSRPAVPAAAQPPVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
              |||:|||||
a025      KAAAVKSRPAVPAAAQPLVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
              160     170     180     190     200     210

              160     170     180     190     200     210
m025.pep      DNMLSIGQIVKVKPAGYAAPKTA AVESRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
              || |||:|||||
a025      DNTLSIGQIVKVKPAGYAAPKAAVKS RPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
              220     230     240     250     260     270

              220     230     240     250     260     270
m025.pep      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQ GKVVADFGGNNKGVDIAGNAGQPVLAAD
              |||:|||||

```

```

a025      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLAAD
           280      290      300      310      320      330

m025.pep      280      290      300      310      320      330
GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDASRT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a025      GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTASRT
           340      350      360      370      380      390

m025.pep      340      350
QLHFEVRQNGKPVNPNSYIAFX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a025      QLHFEVRQNGKPVNPNSYIAFX
           400      410

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 025 shows 75.6% identity over a 353 aa overlap with a predicted ORF (ORF 025.ng) from *N. gonorrhoeae*:

m025/g025

```

m025.pep      10      20      30
VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      GMQTVSSAPVYNPYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
           40      50      60      70      80      90

m025.pep      40      50      60      70      80      90
YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
           100     110     120     130     140     150

m025.pep      100     110     120     130     140     150
KAAAVKSRPAVPAAAQPPVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMT
|
g025      K-----

m025.pep      160     170     180     190     200     210
DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      -----TAAVESRPAPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
           160     170     180     190

m025.pep      220     230     240     250     260
KAVPAPAP--QSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
           200     210     220     230     240     250

m025.pep      270     280     290     300     310     320
ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g025      ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
           260     270     280     290     300     310

m025.pep      330     340     350
RTQLHFEVRQNGKPVNPNSYIAFX

```

g025 |||||
 RTQLHFEVRQNGKPVNPNSYIAFX
 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC
 51 TGACAATTTT CTTTTCGCC AGCCAAATAT CATGCGTATC TTTCGGTTCG
 101 GGCTTGTTGG GCATGGCAAC CTTCAACAGC CGCGCCATCA CAGGAATCGT
 151 CGTTCCCTGA ATCAGCAGCG ACAGACCAC CACGGCAAAC GCCACATCAA
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC
 301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCCGCCCTG
 401 TCCAACACGC CGGCGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT
 451 TGCCTGCGCC AGCCAAGCCA AACCGTCCAT CACACGCAA ACCTGTTCG
 501 TcgCACGGTT GCGCTGGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC
 551 AAAAAGCCGC TGCCGCCTAT GGTATTGGTA AACGCAACA CAAGCAGCCC
 601 GCCCGACACA ATCATCAGCG CGTACAGACC TTCCGtacac acctccaatt
 651 cccaatcaac gtcataagctg tctcccgtgt taaaatgttc ttcacttcag
 701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta naccctgggg
 751 tgccccaacg gatttagtaa cctcccaatg actctgcttg tcgccccctt
 801 cgcccgcttt ctccttcagg gaaaacttgt tgtccccgtc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep
 1 MVSLRFRFGN HFKRRHSDNF LFRQPNIMRI FRFGLVGHGN LQQRHHRNR
 51 RSLNQQRQHH HGKRHIKQV RIGNAHQHRH HRQRNRYGSS QAQPTDIRLF
 101 TQAVIEFPQT AEHCQRTDQ HQERRNRQGF RRPVQHAGGR NQQTTEHDEQS
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNROKAAAAY GIGKRKHKQP
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPPSSQ PETFMCXTLG
 251 CPNGFSNLPM TLLVAPFARF LLPGKLVVPV LH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTT TATTCGGCTA TACGCCTTTT
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CCGCCGCCCT
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAAACGTG
 201 CGGACAAAGT GGTGGAACC ACGCTCAGAA ACAACAGTGC GCCACCCGGC
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)
 1 ...RLKHGVLHF YSAIRLFTQA VIEFPQTAEH CRRTRDQHQE RRRNQGFRRP
 51 VQHVGRRNQQ QRHSQTCGQS GRNHAQKQQC ATRQ....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq
 1 ATACGCCTTT TCACGCAGGC TGTAAATGAA TTTCCACAAA CCGCCGAACA
 51 CTGCCGGCGG ACGCGCGACC AGCATCAGGA ACGCCGCAAT CGCCAAGGCT
 101 TCCGCCGCCG CGTCCAACAC GTTGGCAGGA GAAACCAGCA GCAAAGGCAT
 151 TCCCAAACGT GCGGACAAAG TGGTCGAAAC CACGCTCAGA AACAACAGTG
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)
 1 IRLFTQAVIE FPQTAEHCRN TRDQHQRERN RQGFRRPVQH VGRRNQQQRH
 51 SQTGQSGRN HAQKQQCATR Q

210

m031/a031 100.0% identity over a 71 aa overlap

	10	20	30	40	50	60
m031.pep	RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH	CRRTDQHQ	ERRNRQGFRR	PVQHVGRNQ
a031		IRLFTQAVIE	FPQTAEHCR	RTRDQHQE	RRNRQGFRR	PVQHVGRNQ
		10	20	30	40	

	70	80
m031.pep	QRHSQTCG	QSGRNHAQKQ
a031	QRHSQTCG	QSGRNHAQKQ
	50	60

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

		10	20	30
m031.pep		RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH
		:: :	:	
g031	NQQRQHHG	KRHIKQQV	RIGNAHHQ	RHRQRNRYG
	60	70	80	90

	40	50	60	70	80
m031.pep	CRRTDQHQ	ERRNRQGFRR	PVQHVGRNQ	QQRHS-QTCG	QSGRNHAQKQ
	:		:	:	:
g031	CQRTDQHQ	ERRNRQGFRR	PVQHAGGRNQ	TEHDEQSCL	RQPSQTVHHTQ
	120	130	140	150	160

g031	TDNDAGKV	NRQKAAA	YGIGKRKH	KQPARHNN	QRVQTFRTH
	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

```

1  ATGCGGCGAA  ACGTGCCTGC  CGTCGCCGTA  TTGCGCCGCC  CACGATTCTGA
51  GGCGTTTTTG  GATTGGCGGT  TGGCTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101  AACAGGGCTT  TGCCGTCCGA  TGCCGTCTGA  CGCAGCGGCA  GATAGTTTTT
151  CAAGGCTTCC  ACGCTTTTGC  CGGTCAGCGG  AACCTGACGC  TGCTTGCGCC
201  CTTTGCCGGT  AACGTGTACC  CACGCTTCGT  CCAAATATAC  ATCATCTGCA
251  TTCAAGCCGT  GTATCTCGCT  CACGCGCAAA  CCGCTGCCGT  ACATCAGCTC
301  GAACAGCGCG  TGGTCGCGCA  CCGCCAGCGG  GTCGCGCCCG  TCCACGGGCA
351  AATCCAACAT  CCGGTTTCAG  CATTCCTGCG  GCAGGGCTTT  GGGTACGCGC
401  TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  CGCGCATCAG
451  CCGCGGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCACGCC  GACAGCTTGC
501  GCGCCAGCGT  CCGACCGTCC  AAACCGCGCT  GCGACAGCCG  CCGCAACGCC
551  GccgTAAAA  CGCGCCGCGA  CAAGTCCTGC  GGCACGCgc  ctgcaTCTTC
601  AGACGGCATT  TGTGCCAACA  GTGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651  ATGCCGCAAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701  TAAGCGTCAA  AATAcgcgc  AAACccgTCC  AAAACCATAA  CCGTCCCACA
751  CAAATATCAA  AAAACCACTG  A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

g032.pep

```

1  MRRNVPVAV  LRRPRFEAF  L  DLALAQARAV  PAGKQGFVR  CRLTQRQIVF
51  QGFHAFAGQ  R  NLTLAPFAG  N  NVYPRFVQIY  IICIQAVYLA  HAQTAAVHQL

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```

101 EQRVVAHRQR VAAVHGQIQH PVQPFLRQGF GYALGLLRRF DVGGRVGAHQ
151 PAFDQPGAIL PPRRQLARQR PTVQTLARQP PQRRLKIAPR QVLRHAACIF
201 RRHLCQQCKQ FFQIAPVCRN RVLRLALAH D VFQISVKIRR KPVQNHNRPT
251 QISKNQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

m032.seq (partial)
1 ATGCGGCGAA ACGTGCmTGC mGTGCCCGTT kTGCGCCGCC CATTGCGCCA
51 AACGTTTTTG GATTGGCGT TGGCTCAGGC GCGTGCCGT CCGTCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGACCAGCGG CACCTGCCGC TgTT.GCGCC
201 CTTTGCCGAT AACGTGTACC CACGCTCGT CCAAATAGAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGGGCG TGGTCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTCAGC CATTCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG CGTGCATCAG
451 GCCGCGCTTT ACCAGCCAAA CGCAATACTG CCGCCAAGAC GAAAGCTTGC
501 GAGCCAGCGT CCGTTCCTCC AAACCGCG...

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```

m032.pep (partial)
1 MRRNVXAVAV XRRPLRQTFE DLALAQARAV PAGKQGFVAV CRLTQRQIVF
51 QGFHAFADQR HLPLXAPFAD NVYPRXVQID IICIQAVYLA HAQTAAVHQF
101 EQGVVAHRQR VAAVHGQIQH PVQPFLRQGF GYALGLLRRF DVGGRVGVHQ
151 AALYQPNAIL PPRRKLASQR PFPQTA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```

a032.seq
1 ATGCGGCGAA ACGTGCCTGC CGTCGCCGT TTGCGCCGCC CATTGCGCCA
51 AACGTTTTTG GATTGGCGT TGGCTCAGGC GCGTGCCGT CCGTCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGGTCAGCGG AACCTGCCGC TGCTTGCGTC
201 CTTTGCCGCT AACGTGTACC CACGCCTCGT CCAAATATAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGCGCG TGATCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTCAGC CATTCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG TATGCAGCAG
451 ACCGCGTTTG ACCAGCCAGG CGCAATACTG CCGCCAAGAC GACAGCTTGC
501 CCGCCAGCGT CCGCGCATTC AAACCGCGCT GCGACAGCCG CCGCAACGCC
551 GCCGTAAAT CGCGTGTGCA CAAGCCCTGC GGCACGCCG CTGCATCTTC
601 AGACGGCATT TGTGCCAACA GCGCAAACAG TTCTTCCAAA TCGCGCCGCT
651 ATGCCGCCAC CGTGTGCTCC GACTTGCCCT CCGGCACGAT GTTTTCCAAA
701 TAAGCGTCAA AATGCGCCGC AAACCCGTCC AAAACCATAA CCGCCCCACA
751 CAAATATCAA AAAACAGTG A

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```

a032.pep
1 MRRNPAVAV LRRPLRQTFE DLALAQARAV PAGKQGFVAV CRLTQRQIVF
51 QGFHAFAGQR NLPLASFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHQF
101 EQRVIAHRQR VAAVHGQIQH PVQPFLRQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGAIL PPRRQLARQR PRIQTALRQP PQRRLKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAH D VFQISVKMRR KPVQNHNRPT
251 QISKKQ*

```

m032/a032 88.1% identity over a 176 aa overlap

```

          10      20      30      40      50      60
m032.pep  MRRNVXAVAVXRRPLRQTFDLALAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFADQR
          ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||
a032      MRRNPAVAVLRRPLRQTFDLALAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFAGQR
          10      20      30      40      50      60

```

212

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVA AVHGQIQH					
a032	NLPLLASFAGNVYPRLVQIYIICIQAVYLAHAQTAAVHQFEQRVIAHRQRVA AVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFQTA					
a032	PVQPFLLRQGFYALGLLRRFDVGGRVGMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVLRRLALAHDFVQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFLDLALAQAARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFADQR					
g032	MRRNVPAVAVLRRPRFEAFDLDLALAQAARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVA AVHGQIQH					
g032	NLTLLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQFEQRVVAHRQRVA AVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFQTA					
g032	PVQPFLLRQGFYALGLLRRFDVGGRVGAHQPAFDQPGAILPPRRQLARQRPPTVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCQCKQFFQIAPVCRNRVLRRLALAHDFVQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

1	ATGGCGGCGG	CGGACAAACT	CTTGGGCGGC	GACCGCCGCA	GCGTCGCCAT
51	CATCGGAGAC	GGCGCGATGA	CGGCGGGGCA	GGCGTTTGAA	GCCTTGAATT
101	GCGCGGGCGA	TATGGATGTG	GATTGTCTGG	TCGTCTCTCA	CGACAACGAA
151	ATGTCGATTT	CCCCAACGT	CGGCGCGTTG	CCCCAATATC	TTGCCAGCAA
201	CGTCGTGCGC	GATATGCACG	GACTGTTGAG	TACCGTCAAA	GCGCAAAcgg
251	GCAAGGTATT	AGACAAAATA	CCCGGCGCGA	TGGagtTTGC	CCAAAAAGTC
301	GAACAcaaaA	TCAAAACCCT	TGCCGAAGAA	GCCGAACACG	CCAAACAGTC
351	GCTGTGCTG	TTTGAAAATT	TCGGCTTCCG	CTACACCGGC	CCCGTGGACG
401	GACACAACGT	CGAGAATCTG	GTGGACGTAT	TGAAAGACTT	GCGCAGCCGC
451	AAAGGCCCTC	AGTTGCTGCA	CGTCATCACC	AAAAAGGGCA	ACGGCTACAA
501	ACTCGCCGAA	AACGACCCcg	tcaAATACCA	CGCCGTCGcC	aACCTGCcta
551	AAGAAGGCGG	GGCGCAAATg	ccGTCTGAAA	AAGAACCCAA	GCCCCGcGcC
601	aaaccgACCT	ATACCCAAGT	ATTGGGCAAA	TGGCTGTGCG	ACCGGGCGGC
651	GGCAGATTCC	CGACTGGTTG	CGATTACCCC	CGCCATGCGC	GAGGGCAGCG

```

701  GACTGGTGGA  GTTTGAACAA  CGATTCCCCG  ACCGCTATTT  CGATGTCGGC
751  ATCGCCGAGC  AGCACGCCGT  tacCTTTGCC  GGCGGTTTGG  CGTGCGAAGG
801  CATGAAGCCC  GTCGTGGCGA  TTTATTCCAC  CTTTTTACAA  CGCGCCTACG
851  ACCAACTGGT  GCACGACATC  GCCCTGCAAA  ACCTGCCCGT  TTTGTTTGCC
901  GTCGACCGTG  CGGGCATCGT  CGGCGCGGAC  GGTCCGACCC  ATGCCGGCTT
951  GTACGATTTG  AGCTTCTTGC  GCTGTGTGCC  GAACATGATT  GTTGCCCGCG
1001 CGAGCGATGA  AAACGAATGC  CGCCTGCTGC  TTTGACCTG  CTATCAGGCG
1051 GATGCGCCCG  CCGCCGTCCG  CTATCCGCGC  GGCACGGGTA  CGGGCGCGCC
1101 GGTTTCAGAC  GGCATGGAAA  CCGTGAAAT  CGGCAAGGGC  ATTATCCGCC
1151 GCGAAGGTGA  GAAAACCGCC  TTcatTGCCT  TCGGCAGTAT  GGTCCGCCAC
1201 GCATTGGCGG  TTGCCGAAAA  ACTGAACGCC  ACCGTCGCCG  ATATGCGCTt
1251 cgtcaaacCG  ATAGACGAAG  AGTTGATTGT  CCGCCTTGCC  CGAAGCCAcy
1301 accGCATCGT  TACCCTTGAA  GAAAACGCCG  AACAGGGCGG  CGCAGGCGGC
1351 GCGGTCTTGG  AAGTGTGGC  GAAACACGGC  ATCTGCAAA  CCGTTTTGCT
1401 TTTGGGCGTT  GCCGATACCG  TAACCGAACA  CGGCGATCCG  AAAAACTTT
1451 TGGACGATTT  GGGTTTGAGT  GCCGAAGCGG  TGAACGCCG  GGTGCGCGAG
1501 TGGCTGCCGG  ACCGTGATGC  GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

g033.pep

```

1  MAAADKLLGG  DRRSVAII  GD  GAMTAGQAFE  ALNCAGDMDV  DLLVVLNDNE
51  MSISPNVGAL  PKYLASNVR  DMHGLLSTVK  AQTGKVLDKI  PGAMEFAQKV
101 EHKIKTLAEE  AEHAKQSL  SL  FENFGFRYTG  PVDGHNVENL  VDVCLKDLRSR
151 KGPQLLHVIT  KKGNGYKLA  E  NDPVKYHAVA  NLPKEGGAQM  PSEKEPKPAA
201 KPTYTQVFGK  WLCDRAAAD  S  RLVAITPAMR  EGSGLVEFEQ  RFPDRYFDVG
251 IAEQHAVTFA  GGLACEGMK  P  VVAIYSTFLQ  RAYDQLVHDI  ALQNLPLVLF
301 VDRAGIVGAD  GPTHAGLYD  L  SFLRCVPNMI  VAAPSDENEC  RLLLSTCYQA
351 DAPAAVRYPR  GTGTGAPVS  D  GMETVEIGKG  IIRREGEKTA  FIAFGSMVAT
401 ALAVA EK LNA  TVADMRFVK  P  IDEELIVRLA  RSHDRIVTLE  ENAEQGGAGG
451 AVLEVLAKHG  ICKPVLLLG  V  ADTVTEHGDP  KKLLDDLGLS  AEAVERRVRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

m033.seq

```

1  ATGGCGGCGG  CAGACAACT  CTTGGGCAGC  GACCGCCGCA  GCGTCGCCAT
51  CATCGGCGAC  GGC GCGATGA  CGGCGGGGCA  GGCGTTTGAA  GCCTTGAATT
101 GCGCaG.CGA  TATGGATGT  r  GATTTGCTrG  TCGTCCTCAA  CGACAACGAA
151 ATGTGCGATTT  CCCCCAACGT  CGGCGCGCTG  CCGAAATACC  TTGCCAGCAA
201 CGTCGTGCGC  GATATGCACG  GCCTGTTGAG  TACCGTCAAA  GCGCAAAACGG
251 GCAAGGTATT  AGACAAAATA  CCCGGCGCGA  TGGAGTTTGC  CCAAAAAGTC
301 GAACACAAAA  TCAAAACCTT  TGCCGAAGAA  GCCGAACACG  CCAAAACAGTC
351 GCTGTCTTTG  TTTGAAAACT  TCGGCTTCCG  CTACACCGGC  CCCGTGGACG
401 GACACAACGT  CGAAAATCTG  GTGGACGTAT  TGAAAGACTT  GCGCAGCCGC
451 AAAGGCCCTC  AGTTGCTGCA  CGTCATCACC  AAAAAGGGCA  ACGGCTACAA
501 ACTCGCCGAA  AACGACCCCG  TCAAATACCA  CGCCGTCGCC  AACCTGCCTA
551 AAGAAAGCGC  GGC GCAAATG  CCGTCTGAAA  AAGAACCCTA  GCCGCGCGCC
601 AAACCGACCT  ATACCCAAGT  GTTCGGCAAA  TGGCTGTGCG  ACCGGGCGGC
651 GGCAGATTCC  CGACTGGTTG  CGATTACCCC  CGCCATGCGC  GAGGGCAGCG
701 GCTTGGTTGA  GTTTGAACAA  CGATTCCCCG  ACCGCTATTT  CGATGTCGGC
751 ATCGCCGAGC  AGCACGCCGT  TACCTTTGCC  GGCGGTTTGG  CTTGCGAAGG
801 GATGAAGCCC  GTCGTGGCGA  TTTATTCCAC  CTTTTTACAA  CGCGCCTACG
851 ACCAACTGGT  GCACGACATC  GCCCTGCAAA  ACCTACCCGT  TTTGTTTGCC
901 GTCGACCGCG  CGGGCATCGT  CGGCGCGGAC  GGCCCGACCC  ATGCCGGTCT
951 GTACGATTTG  AGCTTTTTCG  GCTGCGTGCC  GAACATGATT  GTCGCGCGC
1001 CGAGCGATGA  AAACGAATGC  CGCCTGTTGC  TTTGACCTG  CTATCAGGCA
1051 GACGCGCCCG  CCGCCGTCCG  CTATCCGCGC  GGCACGGGTA  CGGGCGCGCC
1101 GGTTTCAGAC  GGCATGGAAA  CCGTGAAAT  CGGCAAGGGC  ATTATCCGCC
1151 GCGAAGGTGA  GAAAACCGCA  TTCATTGCCT  TCGGCAGTAT  GGTGCGCCCC
1201 GCATTGGCGG  TTGCCGAAAA  ACTGAACGCC  ACCGTCGCCG  ATATGCGCTT
1251 CGTCAAACCG  ATAGACGAAG  AGTTGATTGT  CCGCCTTGCC  CGAAGCCACG

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1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pep

```

1 MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHAIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLDLRSR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAP
401 ALAVAELKNA TVADMRVFKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLGLV ADTVTGHGDP KKLLDDLGLS ABAVRRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1 ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GCGCGATGA CGGCGGTCA GCGGTTTGA GCCTTGAAC
101 GCGCGGCGA TATGGATGTG GATTGCTGG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGT CGGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAAGTC
301 GAACATAAAA TCAAACCCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 ACTGCTTTTG TTTGAAAAC TCGGCTTCCG CTATACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTCGATGTAT TGAAGACCT GCGCGGACGC
451 AAGGCGCCGC AGCTTCTGCA CGTCATCAC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GGCGCAAATG CCGTCTGAAA AAGAACCCAA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGCG
651 GGCAGATTCC CGACTGTTG CGATTACCC CGCATGCGC GAGGCGAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCAGCGCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTTGGC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCGGTTT
951 GTACGATTTA AGCTTTTTC GCTGCATTCC GAATATGATT GTCGCGCGC
1001 CGAGCGATGA AAATGAATGC CGCTGCTGC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGTGCC
1101 GGTTCAGAC GGCATGAAA CCGTGAAAT CGGCAAGGGC ATTATCCGCC
1151 CGAAGGTGA GAAACCGCA TTCATTGCCT TCGCAGTAT GGTGCGCCCT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCC ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG
1301 ACCGCATCGT TACCCTTGAA GAAAACGCC AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT CCGGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pep

```

1 MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHAIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLGR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREG EKTA FIAFGSMVAP
 401 ALAVAGKLNA TVADMRVVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS
 451 AVLEVLAKHG ICKPVLLLG V ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
 501 WLSDRDAAN*

m033/a033 98.4% identity over a 509 aa overlap

	10	20	30	40	50	60
m033.pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISP NVGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISP NVGAL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m033.pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m033.pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPVDGHNVENLVDVLEDLRGRKG PQLLHVITKKGNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m033.pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m033.pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m033.pep	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
	370	380	390	400	410	420
m033.pep	GTGTGAPVSDGMETVEIGKGIIRREG EKTA FIAFGSMVAPALAVAEKLNATVADMRVVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREG EKTA FIAFGSMVAPALAVAGKLNATVADMRVVKP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m033.pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLG VADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGS AVLEVLAKHGICKPVLLLG VADTVTGHGDP					
	430	440	450	460	470	480
	490	500	510			
m033.pep	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSI SPNVGAL	60
g033	MAAADKLLGGDRRSVAIIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSI SPNVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPLLHVITKKGNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAADSRLVAITPAMREGSGLVEFEQ	240
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAADSRLVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGFSMVAPALAVA EKL NATVADMR FVKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGFSMVATALAVA EKL NATVADMR FVKP	420
m033 . pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGI CKP V L L L G V A D T V T G H G D P	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGI CKP V L L L G V A D T V T E H G D P	480
m033 . pep	KKLLDDLGLSAEAVERRVRAWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVREWLPRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

1	ATGAGCCGTT	TATGGTTTTT	TGCCGTAAAA	AACATTATAA	TCCGCCTTAT
51	TTACCTATTG	CCCAAGGAGA	CACAAATGGC	ACTCGTATCC	ATGCGCCAAC
101	TGCTTGACCA	CGCCGCCGAA	AACAGCTACG	GCCTGCCCGC	GTTCAACGTC
151	AACAACCTCG	AACAAATGCG	CGCCATTATG	GAAGCCGCCG	ACCAAGTCAA
201	CGCGCCCGTC	ATCGTACAGG	CGAGCGCAGG	TGCGCGCAAA	TACGcggGCG
251	CGCCGTTTTT	GCGCCACCTG	ATTCTGGCGG	CAGTCGAAGA	ATTTCCGCAC
301	ATCCCCGTCG	TGATGCACCA	AGACCACGGC	GCATCGCCCG	ACGTgtgCCA
351	ACGCTCCATC	CAACTGGGCT	TCTCCTCCGT	GATGATGGAC	GGCTCTTTGC
401	TCGAAGACGG	CAAAACCCCT	TCTTCTTACG	AATACAACGT	CAACGCCACC
451	CGTACCGTCG	TCAACTTCTC	CCACGCCTGC	GGCGTGTCCG	TCGAAGGCGA
501	AATCGGCGTA	TTGGGCAACC	TCGAAACCGG	CGAAGCAGGC	GAAGAAGACG
551	GAGTGGGCGC	GGCAGGCAAA	CTCTCACACG	ACCAAATGCT	CACCAGCGTT
601	GAAGATGCCG	TGCGTTTCGT	TAAAGATACC	GGCGTTGACG	CATTGGCGAT
651	TGCCGTCGGC	ACCAGCCACG	GCGCATACAA	ATTACCCCGT	CCGCCACACG

```

701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCTGTT TCGTTGGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAIP IVQASAGARK YAGAPFLRHL ILAAVEEFPF
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLLEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRVFKDT GVDALAIIVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKI NEYGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA WACAGCTACG GCyTGCCGGC GTTCAACGTC
151 AACAACTCG WACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGCGCG CTGTCGAAGT ATTTCCACAC
301 ATCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTCTC CCACGCTTGC GCGGTATCCG TTGAAGGCGA
501 AATCGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGGTTGACG CATTGGCTAT
651 TGCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETQMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLXQMRAIM EAADQVDAPV IVQASAGARK YAGAPFLRHL ILAAVEVFPF
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAIIVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGCGCG CTGTCGAAGA ATTTCCGCAC
301 ATCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCC ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TTTCTCCGT GATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

```

```

451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GGCCTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TGCCTTTCGT TAAAGATACC GGCCTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCGTACAA ATTCACCCGT CCGCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTTCCACC GCGCGGTAC GCCGTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GCTACCTCG GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

```

a034.pep
1  MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRVFKDT GVDALAIAGV TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

```

          10      20      30      40      50      60
m034.pep  MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM
          || |||||:|||||
a034      MSRLWFFAAKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM
          10      20      30      40      50      60

          70      80      90      100     110     120
m034.pep  EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI
          |||||:|||||
a034      EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHPVVMHQDHGASPDVCQRSI
          70      80      90      100     110     120

          130     140     150     160     170     180
m034.pep  QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGDAG
          |||||:|||||
a034      QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGEAG
          130     140     150     160     170     180

          190     200     210     220     230     240
m034.pep  EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
          |||||:|||||
a034      EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
          190     200     210     220     230     240

          250
m034.pep  RIKEIHQALPNTHIVMH
          |||||
a034      RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN
          250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

m034/g034

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILA AVEVFPHIPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILA AVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034 . pep	QLGFSSVMMDGSLMEDGKTPSSYEYNVNATRTVNVNFSHACGVSVEGEIGVLGNLETGDAG	180
g034	QLGFSSVMMDGSLLEDGKTPSSYEYNVNATRTVNVNFSHACGVSVEGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPOEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

g036 . seq

1	ATGCTGAAGC	CGTGTTTGGT	ATACAGTGCC	TGTGCGGCGG	cgttgccTGC
51	GCGGACTTCG	AGCAGCAGGC	GTTGCGTGCC	TTCGGGCAGA	TGTGCGTACC
101	AATATTCGAG	CAGGGCGGAC	GCAACGCCCC	GTCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAGTTC	GGATTTCGTC	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCTGCCGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	GCGAAACAAG	CGCGGACTCA	AATTGGCGTT	GCGTCCACGC	GGACGGGTTG
301	CAGACGGTAT	CGAGCGCGGC	CAGTGCAGCG	CAGTCCGACG	GTGAGGCTGG
351	GCGGATGTTT	ATGTTTCGTG	CTTCCGTTCC	GCCTGTTCTT	TGGCAGTCAG
401	GGCGATTTTG	TTGCGGACGT	AGAGCAGTTC	GGCGTGTGCC	GCGCCAGTTG
451	CGGGATAGCC	GCCGCCGAGG	GCGAGCGCGA	GAAAATCGGC	GGCGGTCCGC
501	ATATCGGGTT	TGCCTGAGAA	GGGCGGACGG	TTTTCAGTG	CGAACGCACT
551	CGCGATGCCG	TCTGAAAAGA	CGTACCCCTC	GGGGAGGGCA	ATGTCTGCCG
601	CCCTACCGAC	TTGATAATCG	CTCAAACGGC	GGCGGTTTCA	CGTGTCCGAA
651	CACGCATAAA	ACACTTCGCC	CATACGCGCG	TCCGAGCGCG	CGAGTATGCA
701	GCTTTGCGGC	GGCGGCAGCG	AGGCGGCGGC	ATCGAGCGTG	GGGATGCCGA
751	TTAAAGGCGT	GTCGAACGGC	GTTGCCAAAC	CTTGCGCCAC	GCCGATGCCG
801	ATACGCAGTC	CGGTAA			

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

g036 . pep

1	MLKPCLVYSA	CAAALPARTS	SSRRCVPSGR	CAYQYSSRAD	ATPRRRHSGA
51	VAIRCSSDSS	GRFCQTIKAA	ILPSFSARKT	CSDGETSADS	NWRCVHADGL
101	QTVSSAASAA	QSDGEAGRMF	MFVPSVPPVL	WQSGRFCCGR	RAVRRVPRQL
151	RDSRRRGRAR	ENRRRSAYRV	CLRRADGFPV	RTHCRCRLKR	RTPRGGQCLP
201	PYRLDNRSNG	GSACRTTHK	TLRPYARPQR	RVCSFAAAAA	RRRHRAWGCR
251	LKACRTALPN	LAPRRCRYAV	R*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

m036 . seq

1	ATGCTGAAGC	CGTGCGCCGT	GTACAGTGCC	TGTGCGGCGG	TGTTGCCTGC
51	ACGGACTTCG	AGCAGCAGGC	GTTGCGTGTC	TTCGGGCAGA	TGTGTGAACC
101	AATATTCGAG	CAGGGCGGAC	GCAATTCCTT	GGCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAGTTC	GGATTTCGTC	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCCg . CGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	GCGAAACCAG	TGCGGACTCA	AATTGGCGTT	GCGTCCATGC	GGACGGGTTG
301	CAGACGGCAT	CGAGTGCAGC	CAGCTCCTCA	CAATCGGCAC	AAACGGCACG

220

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351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CATAAGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GGCAGCGAGC AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

```

m036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPLWPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

```

a036.seq
1 ATGCTGAAGC CGTGCCCGT GTACAGTGCC TGTGCGGCGG TGTTCCTGCG
51 ACGGACTTCG AGCAGCAGGC GTTGCGTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GGCAGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCGCCGT CTTTTTCCGC AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGGCGCGC CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GGCGATTTTG TTGCGGACGT AGAGCAGCTC GGCGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGGC GGCAGTCCGC
501 ATATCGGGTT TGCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 CCCGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GGCAGTTCAG CGTGTGCAAC
651 CATGCATAAA ACACTTCGCC CATAAGAGCG TCCGAGCGCG CAAGGATGCA
701 GCTTTGCGGC GGCAGCGAGC AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAAGGAGT ATCAAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

```

a036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRRFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCRLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

```

          10      20      30      40      50      60
m036.pep MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRRHSGAVAI RCSSDSS
          |||
a036      MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRRHSGAVAI RCSSDSS
          10      20      30      40      50      60

          70      80      90     100     110     120
m036.pep GRFCQTIKAAIPXSFSAKRTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF
          |||
a036      GRFCQTIKAAIPPSFSAKRTCS DGETSADSNWRCVHADGLQTASSAASAAQSAXTARRMF
          70      80      90     100     110     120

```

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	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCLRTAELLPA					
a036	TGAPSVPPVLWQSGRFCCGRRARRVPQRRRENRLQPPDXGSRRRSAYRVCLRRADGFPA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSEFAAAAA					
a036	RTHCRCLKRRILPAAGCLPPDRPDNRSNGGGSACRTMHKTLRPYVRPQRQGCSEFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRRLRGYQTALPNPELHRCRYAVRX					
a036	RRRHRARVRRLKEYQTALPNLAPRRCRYAVPX					
	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRRHSGAVAIRCSSDSS					
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAYQYSSRADATPRRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m036.pep	GRFCQTIKAAIPXSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
g036	GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCLRTAELLPA					
g036	MFVPSVPPVLWQSGRFCCGRRARRVPQRLRDSRRRGRARENRRRSAYRVCLRRADGFVP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSEFAAAAA					
g036	RTHCRCLKRRTPRGGQCLPPYRLDNRSNGGGSACRTTHKTLRPYARPQRRVCSFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRRLRGYQTALPNPELHRCRYAVRX					
g036	RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTTCCTGTC
51  ACGGACTTCG AGCAGCAGGC GTTGC GTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCGA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCT GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCGCGCGT CTTTTCCTGC AAGGAAAACC TGTTCGGACG
251 GCGAAACAG TGCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGC GGC CAGCTCCTCA CAATCGGCAC AAACGGCACG

```

```

351  GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401  GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCGTGTGCG GCATGGACGG
451  CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501  ATATCCGCTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551  GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601  CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651  CATGCATAAA AACTTCGCC CATAAGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```

m036-1.pep
  1  MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
 51  VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101  QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151  QDNRPWLPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201  PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

```

              10      20      30      40      50      60
m036-1.pep  MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIIRCSSDSS
g036        MLKPCLVYSACAAALPARTSSSRRCVPSGRCAIYQYSSRADATPRRRHSGAVAIIRCSSDSS
              10      20      30      40      50      60

              70      80      90      100     110     120
m036-1.pep  GRFCQTIKAAIPPSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF
g036        GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF
              70      80      90      100     110     120

              130     140     150     160     170     180
m036-1.pep  TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMRESRRQSAYPVCLRTAELLPA
g036        MFVPSVPPVLWQSGRFCCGRRARRVPRQLRDSRRRGRARENRRRSAYRVCLRRADGFPV
              130     140     150     160     170     180

              190     200     210     220     229
m036-1.pep  RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERPX
g036        RTHCRCLKRRTPRGQCLPPYRLDNRSNGGGSACRTTHKTLRPYARPQRRVCSFAAAAA
              190     200     210     220     230     240

g036        RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

```

g038.seq
  1  ATGACTGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GGCGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151  AAATTCTATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GGCGGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTGCGGCGCG CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTT CGCCGGCACA TCCGTACGCG
401  AATCAATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAAATTGT CCGCCGTTCA
501  GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATCCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GCACCTACCG CCGGCAGTAC GCGGTAGAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
1   MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
51  KFYAQSIIES GIRFDMLEFG AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDRGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GKLSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
1   ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
51  TTTGAAATTC GGCGAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151 AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501 GGAAGTGGAA AAACAATACG GCTGCCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
1   MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
51  KFYAQSIIES GIRFDMLEFG AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDHGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
1   ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
51  TTTGAAATTC GGCGAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151 AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501 GGAAGTGGAA AAACAATACG GCCTGCCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
1   MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
51  KFYAQSIIES GIRFDMLEFG AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDHGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

          10      20      30      40      50      60
m038.pep  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA KFYAQSIIES
```

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```

a038      |||||
          10      20      30      40      50      60
          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||
a038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          70      80      90      100     110     120

          130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          |||||
a038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          130     140     150     160     170     180

          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          |||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

m038.pep  10      20      30      40      50      60
          MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
          |||||
g038      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIES
          10      20      30      40      50      60

          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||
g038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
          70      80      90      100     110     120

          130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          |||||
g038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQEVEKQYGLPVAPI
          130     140     150     160     170     180

          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          |||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51  CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCCGCTT
101 CTGGGTCAA GAAAcccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaaagt gtttcgggat gTcaaaCTCG

```

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```

251 TCcaccgcaT cggcacgcac gccattagca aGAaacagat gtcccgcgac
301 gaaatCgccg atatcctcaa cggcggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGCaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

g039.pep

```

1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
51 KNAKGCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGL NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

m039.seq

```

1 ATGCCGTCCG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCT GTGACGAAAT CGCCGGCATT CTCAACGCGG GTACAACCCA
351 GCCCATATT CCGCCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCGCGCCGCG CCCGCCGCTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTTGCCCT TATCGTCCTC ATTATGCAGC TTTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

m039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPPXXXXXX
51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTQPD I PPATAATPAA APQVTVPAA PARQDGFNWT
151 IATLFLALIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

a039.seq

```

1 ATGCCGTCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCAGGAAA
201 GAACCCATAT TCAACGATT. TGCCCGAAGC TGTTTCGGAT GTCAAACCTCG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCGCCG
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTCC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

a039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVL*

```

m039/a039 79.4% identity over a 170 aa overlap

```

              10      20      30      40      50      60
m039.pep      MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNSMSPPXXXXXXXXXXXXXXXXX
              |||
a039           MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNSMSPKASSSAKNAKECLKPK

```

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	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIG	TRAIGKKQISRDEI	AGILNGGTTQ	PDI	
a039	TIWQARKNPYSTIX----	PEAVSDVKLVHRIG	TSAGKKQISRDEI	AGILNGGTTQ	PDI	
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAATPAAAPQVT	PPAAPARQDGFN	WTIATL	FALIVLIMQL	SYLVILX	
a039	PPATAATPAAAPQVT	PPAAPARQDGFN	WTIATL	FALIVLIMQL	SYLVILX	
	120	130	140	150	160	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPD	THEEIPCPV	SAPTAKPV	SGSKKPNS	MSPXXXXXX	XXXXXXXXXXXX
g039	MPSEPPAASDGIKPT	HTTEKTS	CPPVSVRT	AKPASGSK	KPSSTSPK	ASSAKNAKGLKPK
	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIG	TRAIGKKQISRDEI	AGILNGGTTQ	PDI	
g039	TIWQARKNLYSTIG----	PKLFRDVKLVHRIG	THAISKQMSRDEI	ADILNGGTTL	HDT	
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAAT-PAAAPQVT	PPAAPARQDGFN	WTIATL	FALIVLIMQL	SYLVILX	
g039	PPATAAAAPAAAPQV	SVPPA---RQ	EGLNWTIATL	FALIVLIMQL	SYLFILX	
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

```

1  ATGAACGCGC  CCGACAGCTT  TGTCGCCAC  TTCCGCGAAG  CCGCCCCCTA
51  CATCCGCCAA  ATGCGCGGCA  CGACACTGGT  CGCCGGCATA  GAcggCCGCC
101 TGCTCGAAGG  CGGCACCTTA  AATAAGCTCG  CCGCCGACAT  CGGGCTGTG
151 TCGCAACTGG  GCATCCGACT  CGTCCTCATC  CACGGCGCGT  ACCACTTCTT
201 CGAcgCCTC  GCCGCCGCGC  AAGgccGCAC  GCCGCATTAT  TGCCGgggtt
251 tGCGCGTTAC  CGACGaAACc  tcGctcgGAC  AGGCGCAGCA  GtttGCCGCG
301 AccgTCCGCA  GCCGTTTTGA  agcCGCATTG  tgcggcagCG  tttcaggatt
351 cgcgCGCGCG  CCTTCCGTCC  CGCTCGTAtc  gggcaacttc  ctgacCGCCC
401 GTCcgatggg  cgtgattgac  ggaACCGata  tggaaatacgc  gggggttatc
451 cgcaaaaccg  ACACCGCCGC  CCTCCGTTC  CAACTCGACG  CGGGCAATAT
501 CGTCTGGATG  CCGCCGCTCG  GGCATTCCCTA  CGGCGGCAAA  ACCTTCAATC
551 TCGATATGGT  GCAGGCCGCC  GCTTCCGTCTG  CCGTCTCGCT  TCAGGCCGAA
601 AACTCGTTT  ACCTGACCTT  TTCAGACGGC  ATTTCCCGCC  CCGACGGCAC
651 GCTCGCCGAA  ACCCTCTCGG  CACAGGAAGC  GCAATCGCTG  GCGGAACACG
701 CGGCCAGCGA  AACCCGACGA  CTGATTTCTG  CCGCCGTTGC  CGCGCTCGAA
751 GCGGCGTGC  ATCGCGTCCA  AATCCTCAAC  GGGGCCGCCG  ACGGCAGCCT
801 GCTGCAAGAA  CTCTTACCC  GCAACGGCAT  CGGCACGTCC  ATTGCCAAAG
851 AAGCCTTCGT  CTCCATCCGG  CAGGCGCACA  GCGGCGCAT  CCCGCACATC
901 GCCGCCCTCA  TCCGCCCGCT  GGAAGAACAG  GGCGTCTAT  TGCACCCGAG
951 CCGCGAATAC  CTCGAAAACC  ACATTTCGGA  ATTTTCCATC  CTCGAACACG

```



```

1001  ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051  TGGCGCGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGg
1101  ctACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151  GCATAAGCAG GCTGTTCGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201  GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCC AAACGCGGCG
1251  CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301  TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

g040.pep

```

1  MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLGGTL NKLAADIGLL
51  SOLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVDET SLGQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGTLE TLSEAQAQSL AEHAASETRR LISSAVAAL
251 GGVHRVQILN GAADGSLLQE LFTRNGIGTS IAKEAFVSIR QAHSGLDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHDGDLYGC AALKTFEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNPIL VRRLHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

m040.seq

```

1  ATGAGCGCGC CCGACCTCTT TGTCGCCAC TTCCGCGAAG CCGTCCCCTA
51  CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCCGCTC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TCGCGTTTAC GCACGAAACC TCGCTCGAAC AGGCGCAGCA GTTTGCCCGC
301 ACCGTCCGCA GCCGTTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATACGC GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCCCTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCCG CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGGCGGGCA AACCGGACGG CTGATTTCTG CCGCCGAAC CTTCACCCCG
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCGCAywgG G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCCTGCTG CACCGCAs.c GCGAATACCT CGAAAACCAC
901 ATTTCCGAAT TTTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCGC
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAACG CnTGCTTGCC
1051 CACATTATCG ATAAGGCGCG CGGCATAGGC ATAAGCAGGC TGTTGCGACT
1101 GTCCACAAAT ACCGGCGAAT GGTGTGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACCGA
1201 CGGAACTCGC ATATTCTGGT ACGTCGCCCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

m040.pep

```

1  MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLEGDTL NKLAADIGLL
51  SOLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTLSDG ISRPDGTLE TLSEAQAQSL AEHAGGQTRR LISSAELEFTR
251 NGIGTSIAKE AFVSIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

a040.pep

1	MIVPDLFVAH	FREAAPYIRQ	MGRKTLVAGI	DDRLEGGDTL	NKFAADIGLL
51	<u>SQLGIRLVLI</u>	HGARHFLDRH	AAAGQRTPHY	CRGLRVTDET	SLEQAQQFAG
101	TVRSRFEAAL	CQSVSGFARA	PSVPLVSGNF	LTARPIGVID	GTDMEYAGVI
151	RKTDTAALRF	QLDAGNIWVL	PPLGHSYSGK	TFHLDMLQTA	ASVADVSLQAE
201	KLVYLTLSDG	ISRPDGTILV	TLSAQEAQSL	AEHAGGETRR	LISSAVAALE
251	GGVHRVQILN	GAADGSLLEQ	LFTRNGIGTS	IAKEAFVSIR	QAHSGDIPHI
301	AALIRPLEEQ	GILLHRSREY	LENHISEFSI	LEHDGNLYGC	AALKTFEAED
351	CGEIACLAVS	PQAQDSRGYE	RLLAHIIDKA	RGIGISRLFA	LSTNTGEWFA
401	ERGFTASEED	ELPETRKKDY	RSLGRNSHIL	VRLLRH*	

m040/a040 91.5% identity in 436 aa overlap

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLS	QLGIRLVLI				
a040	MIVPDLFVAHFREAAPYIRQMRGKTLVAGIDDRLLEGDTLNKFAADIGLLS	QLGIRLVLI				
	10	20	30	40	50	60
m040.pep	HGARHFLLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAA	LCGSVSGFARA				
a040	HGARHFLLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAA	LCGSVSGFARA				
	70	80	90	100	110	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWL	PPLGHSYS	SGK			
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWL	PPLGHSYS	SGK			
	130	140	150	160	170	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLS	DGISRPDGT	LAETLSAQEAQSLAEHAGGQ	TRR		
a040	TFYLDMLQTAASAAVSLQAEKLVYLTLS	DGISRPDGT	LAETLSAQEAQSLAEHAGGQ	TRR		
	190	200	210	220	230	240

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	190	200	210	220	230	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI					
a040	LISSAVAALGGVHRVQILNGAADGSLQLFTRNGIGTSIAKEAFVSIRQAHSGDIPHI					
	250	260	270	280	290	300
m040.pep	280	290	300	310	320	330
a040	280	290	300	310	320	330
	310	320	330	340	350	360
m040.pep	340	350	360	370	380	390
a040	340	350	360	370	380	390
	370	380	390	400	410	420
m040.pep	400	410				
a040	400	410				
	430					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAAPYIRQMRGTTLVAGIDGRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	120
g040	HGAYHFLDRLAAAQGRTPHYCRGLRVTDETSLGQAQQFAGTVRSRFEAALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALGGVHRVQILNGAADGSLQLFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFEADDCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLYGCAALKTFEADDCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSNGRNSHILVRRRLHRX	413
g040	RSNGRNPILVRRRLHRX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
  1  ATGAGTTCGC CCAAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGCCT
 51  GATTACCGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGTGCGCTGG
101  TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151  GGTTCAAGTT GGACGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201  CAAACGCCGG CTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251  TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301  CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAAGTGC GCG AAACCTCGCC
351  GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401  CCCAACGCGA ATCCGCCGAC AAAGTGCCT GCGTGTGCT GTTTTGTAAA
451  GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
  1  MSSPKHIGLQ GSNNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51  GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101  HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQRESAD KLACVLLFLK
151  EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
  1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
 51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGTGCGCTGG
101  TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151  GGTTCAAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201  CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251  TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301  CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAAGTGC GCG AAACCTCCGC
351  GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401  CCCAACGCGA ATCCGCCGAC GAACTCGCCT GCGTCTTGCT GTTTTGTAAA
451  GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
  1  ISSPEHIGLQ GSNNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101  HPAHALKFYA KLRETSQSW LYSPDGGGHT GNGTQRESAD ELACVLLFLK
151  EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
  1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
 51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATA GGTGCGCTGG
101  TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151  GGTTCAAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201  CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251  TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301  CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAAGTGC GCG AAACCTCGCC
351  GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401  CGCAGCGCGA AGCCGCCGAC GAACTCGCCT GCGTGTGCT GTTTTGTAAA
451  GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
  1  ISSPEHIGLQ GSNNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101  HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQREAA ELACVLLFLK
```

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
a041	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSPQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTQREAADELACVLLFLKEFLGX					
	130	140	150			

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	:	:	:	:	:	:
g041	MSSPKHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRRLGELSPYHNLSDGIDYPPALITTSLSDDRVP					
	PAHALKFYAKLRETS					
	AQSW					
g041	PQKYEACKRRRLGELSPYHNLSDGIDYPPALITTSLSDDRVP					
	PAHALKFYAKLRETS					
	PQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
	:	:	:	:	:	:
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

g041-1.seq

1	ATGAAATCCT	ACCCCGACCC	CTACCGCCAT	TTTGAAAC	TCGATTCCGC
51	CGAAACGCAA	AACTTCGCTG	CTGAAGCGAA	TGCCGAAACG	CGCGCGCGTT
101	TTTTAAACAA	CGACAAGGCG	CGCGCACTTT	CAGACGGCAT	TTTGAATCAA
151	ATGCAGGACA	CCTGGCAGAT	TCCGTTTGTG	CAGGAACACC	CGCGCGCGAT
201	GTACCAATTC	CGTACAAGTG	CGGAATATCC	GAAAGGCGTG	TACCGCATGT
251	GTACGGCGGC	GACCTACCGT	TCCGGCTATC	CCAGTGGGAA	AATCCTGTTT
301	TCGGTGGCGG	ATTTCGATGA	GTTGCTCGGC	GACGATGTGT	ATTTGGGCGG
351	CGTGTGCGAC	TTGGTGGAGC	AGCCCAACCG	CGCGCTGCTG	ACTTTGAACA
401	GAATCGGGCGG	CGATACGGGC	TATACGCTGG	AAGTGGATTT	GGAAGCAGGG
451	AAATTTGGTAG	AGGGCGGTTT	TCACTTTCCG	CGAGGCAAAA	ACCATGTGTC
501	GTGGCGCGAT	GAAAAACAGC	TGTGGGTGTG	TCCGGCTTGG	GACGAACGCC
551	AGTTGACCGA	ATCGGGCTAT	CCGCGCGAAG	TGTGGCTGGT	GGAACGCGGC

```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCTG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CCTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGTCTGAC GCTGCGCAAG GACTGGCACC
851 CCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GCGCGTTTGC CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACGTGGTTTA TCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAACGTACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGTT TCAGACGGCA TCGAAGTGCG
1251 GCAGTTTTCG GCGGTGTCGT CCGACGCGCA ACGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTCGGCA TTCTGAATT GCCGCATTAT CTGGGCAGCG TCGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCAAACATC CGCGGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAC
1501 AAAAGCGTTG ATGATTGTGT GGCAGTCGTG CGTGATTTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGCC
1601 TGATTACCGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CCGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCGC TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCCG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGCG
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGGTGTTGC TGTTTTGTAA
2001 AGAATTTTTG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1  MKSYDPYRHH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51  MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVLVVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDCDVVGYL AGHLLLTLRK DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQP WGGDVVYLAA SDETTPLTLF ALDLNVMELT
401 VMRLQPQFV SDGIEVRQFW AVSSDGERIP YFHVGNKNAAP DTPTLVYAYG
451 GFGIPELPHY LGSVGYWLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGMSS PKHIGLQGS NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1  ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTTCGACGA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGTGTGCGAC TTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCGC CGATACGGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGGCG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTTC CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATT GCGGGTCTCA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

1	MKSYDPDPYRH	FENLDSAETQ	NFAAEANAET	RARFLENDKA	RALSDGILAQ
51	LQDTFQIPFC	QEHRARMYHF	HQDAEYPRKV	YRVCTAATYR	SGYPEWKILF
101	SVADFDELLG	DDVYLGGVSH	LVEQPNRLAL	TLSKLGSDTY	YTLVELDLEAG
151	ELVEGGFHFP	AGKNHVSWRD	ENSVWCPCAW	NEQRLTQSGY	PREVVLVERG
201	KSFEESLPVY	QIGEDGMVMN	AWRYLLDPQS	PIDLIEASDG	FYTKTLVYRVS
251	AEGEAKPLNL	PNDCDVVGYL	AGHLLLTQGS	DWNRANQSPY	SGALVLRKSN
301	RGELGAAQLL	FAPDETQALE	SVETTKRFVV	ASLLENVQGR	LKAWRFADGK
351	WQEVELPRLP	SGALEMTDQP	WGGDDVVYLA	SDFTTPTLTF	ALDLNVMELT
401	VMRQPOQQFD	SDGINVQQFW	TSADGERIP	YFHVKGNAAP	DMPTLVVAYG
451	GFGIPELPHY	LGSIGKYWLE	EGNAFVLNLA	RGGGEFGPRW	HQAQQGISKH
501	KSVDDLLAVV	RLSLERGISS	PEHIGLQGGG	NGGLITAAEP	VREPQSIGAL
551	VCEVPLTDMI	RYPLLSAGSS	WTDPEYGNPQ	YEVCKRRLGE	LSPYHNLSDG
601	IDYPALITEL	SLSDDRVHPA	HALKFYAKLR	ETSAQSWLYS	PDGGGHTGNG
651	TORESASELA	CVLLFLKKEFL	G*		

	10	20	30	40	50	60
m041-1.pep	MKSYDPDYPYRHFNLD	SAETQNF	AAEANAET	RRFL	ENDKAR	ALSDGILAQLQDTRQIPFC
g041-1	MKSYDPDYPYRHFNLD	SAETQNF	AAEANAET	RRFL	NNDKAR	ALSDGILNQMQDTRQIPFC
	10	20	30	40	50	60
	70	80	90	100	110	120
m041-1.pep	QEHRRARMYHFHQDAEY	PKGVYRVCTA	ATYRSGYPEW	KILFSVAD	FDELLGDDVYLGGVSH	
g041-1	QEHRRARMYHFHQDAEY	PKGVYRMCTA	ATYRSGYPEW	KILFSVAD	FDELLGDDVYLGGVSH	
	70	80	90	100	110	120
	130	140	150	160	170	180
m041-1.pep	LVEQPNRALLTSLKLG	SDTAYTLEVD	LEAGELVEGG	FHFHPAGKNH	VSWRDENS	VVWCPCAW
g041-1	LVEQPNRALLTSLKLG	SDTAYTLEVD	LEAGELVEGG	FHFHPAGKNH	VSWRDENS	VVWCPCAW
	130	140	150	160	170	180
	190	200	210	220	230	240
m041-1.pep	NERQLTQSGYPREV	WLVERGKSFEES	LPVYQIGED	GMMVNAWRY	LDPOQGSPID	LIEASDG

Query: 121 LVEQPNRALLTSLKLGSDTAYTTLEVDLEAGELVEGGFHFHPAGKNHVSWRDENS VWVCPAW 180
L N L+ LS G D E D+ GE V+ GF P GK V+W DEN+++V W

Sbjct: 162 LPPTSNLCLIRLSDDGGKADADVREFDIAKGEFVKEGFVLPEGKQSVTWVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNANRYLDPQGSPI 232
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTSSGYAYVTKVVRQSLDQAVEIFRGQKKDVS AERGVLRLDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDWNANQS-YPS 291
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELA FY PNGH---PDTRKVVLP LPTTAVFSGYYKQAIYWLKSDWTS AKGTVFHN 337

Query: 292 GALVAVKLN RGE LGAAQL---LFAPDETQALESVETTKRFVVASLLENVQGR LKAWRFA 347
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIAFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQEVLPRLPSGALEMTDQPWGGDVVYLAASDFTTPTLTLFALDLNVMELTVMRRPOQ 407
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDES DQLFV FSEGFLPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDS DGINVQQFWTTSADGERIPYFHV GKNAAP---DMPTLVYAYGGFGIPELPHYL GSI 464
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAGQISKHKSVDLLAVVRDL SERGISSPEHI 524
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DD AV +DL + ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWH DAGLKTNRQRVYDDFQAVAQDLIAKKVTSTPHL 577

Query: 525 GLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEV C 584
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRPDLWNAVVIQVPLLDVMNFT RMSAGASWQAEYGS PDD-PVE 636

Query: 585 KRRLGELSPYHNLS D GIDYPPALITTSLSDDRVRHPAHALKFYAKLRETS AQSWLYSPDGG 644
 L +SPYHN+ G+ YP TS DDRV P HA K A + + Y G

Sbjct: 637 GAF LRSISPYHNVKAGVAYPEPFETSTKDDRVPVHARKMAALFEDMGLPFFYYENIEG 696

Query: 645 GHTNGTQRESADELACVLLFL 666
 GH +E A A +++

Sbjct: 697 GHAAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1 ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGCAAAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGCGCG ATTTGACGA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTCGCAC CTGGTGGAA AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATT T GGAAGCAGGG
451 GAGTTGGTAG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGAT CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGTTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGACATC TTTTGCTGAC CTTGCGTAAA GACTGCGACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTCTGT GCGAGCCTGC
1001 TGGAAAACGT ACAGGTCGT CTGAAAGCGT GCGCTTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGCGCGCT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CTTGCCGCC AGCGATTTC A
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAACGTGACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCGAATT GCCGCATTAT CTGGGCGACA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GCGGAACATC CGCGCGCGCG

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG AGCGATTGT CCGAACGCGG
1551 TATCAGTTTC CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCGG GTTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TCGGTGTTGC TGTTTTGA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRKH DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPNETQALE SVETTKRFVV ASLLENVQGR LKAWRFTDGK
351 WQETELPRLP SGALEMTDQP WGGDVVYLAA SDFTTPTLTF ALDLNVMELT
401 VMRRQPQQFD SDGINVQQFW TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV SDLSESGISS PEHIGLQGGG NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYDPYRHFENLDSAETQ	NFAAEANAETR	RARFLNNDKAR	ALSDGILAQ	LQDTRQIPFC	
m041-1	MKSYDPYRHFENLDSAETQ	NFAAEANAETR	RARFLNNDKAR	ALSDGILAQ	LQDTRQIPFC	
	10	20	30	40	50	60
	70	80	90	100	110	120
a041-1.pep	QEHRARMYHFHQDAEYPKGV	YRVCTAATYRSGYPEWKILF	SVADFDELLGDDVYLGGVSH			
m041-1	QEHRARMYHFHQDAEYPKGV	YRVCTAATYRSGYPEWKILF	SVADFDELLGDDVYLGGVSH			
	70	80	90	100	110	120
	130	140	150	160	170	180
a041-1.pep	LVEQPNRALLTLSKSGGDTA	YTLEVDLEAGELVEGGFHFP	PAGKNHVSWRDENS	SVWVCPAW		
m041-1	LVEQPNRALLTLSKSGGDTA	YTLEVDLEAGELVEGGFHFP	PAGKNHVSWRDENS	SVWVCPAW		
	130	140	150	160	170	180
	190	200	210	220	230	240
a041-1.pep	DERQLTESGYPREVWLVERG	KSFEESLPVYQIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG		
m041-1	DERQLTESGYPREVWLVERG	KSFEESLPVYQIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG		
	190	200	210	220	230	240
	250	260	270	280	290	300
a041-1.pep	FYTKTYLQVSAEGEAKPLNL	PNDCDVVGYLAGHLLTLRKH	DWHRANQSYR	SGALVAVKLN		
m041-1	FYTKTYLQVSAEGEAKPLNL	PNDCDVVGYLAGHLLTLRKH	DWHRANQSYR	SGALVAVKLN		
	250	260	270	280	290	300
	310	320	330	340	350	360
a041-1.pep	RGELGAAQLLFAPNETQALE	SVETTKRFVVASLLENVQGR	LKAWRFTDGK	WQETELPRLP		
m041-1	RGELGAAQLLFAPNETQALE	SVETTKRFVVASLLENVQGR	LKAWRFTDGK	WQETELPRLP		
	310	320	330	340	350	360

	370	380	390	400	410	420
a041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQQFSDGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQQFSDGINVQQFW					
	370	380	390	400	410	420
	430	440	450	460	470	480
a041-1.pep	TTSADGERIPYFHVGNAAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNAAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
	490	500	510	520	530	540
a041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDDLAVVSDLSERGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
	550	560	570	580	590	600
a041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRRLGELSPYHNLSDG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a041-1.pep	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA					
	610	620	630	640	650	660
	670					
a041-1.pep	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

g042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TGCGGTCGAT GATGAAAATC CAGCCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACGG GCTGCCCCTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGG GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG cggCTTCGCG CTTTTGGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCGG
501 CCCGCCGGTA ATGACAAACT GCGGATTGTG GCGGTGCAGG GATTGCAAT
551 CGGGCTCAAA CAGCGTCCCC ACCGTTGCCG CTTGTCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

g042.pep

```

1  MTMICLRFQA FVPHTSALSN TSTAAGPSCP MAAVRSMMKI QPGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTGSTSPRP
101 LPLAASRFWA NSASICAFNS ATRASLPKIR DRVSICFSPL VRILPLSTVK
151 SMVVAFFANC SYASAPGPPV MTNCGLWRCR DSQSGSNSVP TVAALSNAAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

m042.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCCG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCT
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCCTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

m042.pep

```

1   MTMICLRFOA FVPRTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

a042.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCCG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCT
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCCTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

a042.pep

```

1   MTMICLRFOA FVPRTSALSX TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAAG
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
	130	140	150	160	170	180

```

a042      |||||
          AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

m042.pep      190      200
          ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

m042.pep      10      20      30      40      50      60
          MTMICLRFAQFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL
          |||||:|||||
g042      MTMICLRFAQFVPHTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPGPSL
          10      20      30      40      50      60

m042.pep      70      80      90      100     110     120
          RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
          |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

m042.pep      130     140     150     160     170     180
          AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          |:|||||:|||||:|||||:|||||: || |||
g042      ATRASLPKIRDVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR
          130     140     150     160     170     180

m042.pep      190     200
          ASXSGSNSVPTVAALSNAGCKX
          | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCC ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCT
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCGC CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTC AATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTGTGC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1  MTMICLRFAQ FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCPKADTLL PVT DSTSPR
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
g042	MTMICLRFQAFVPHTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	: : : : : : : : : : :					
g042	ATRASLPKIRDRVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

```

a042-1.seq
1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTCTCTTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCCGT CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTCCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCGCCCGG
501 CCCGCCGTA A

```

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

```

a042-1.pep
1  MTMICLRFQA FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042-1	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

q043.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 177>:

m043.seq

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

m043.per

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/q043

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

a043.seq

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGCCCT CAGCACTTCT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGCGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

242

```

151 GCCGATTTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 ATCCGGCGAC GGTTCGCCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCTGTTA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTGCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGCG
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
  1 MVVSNQNIYA AGPSALLHIR RQKSVMPSER FVEPSRVAVA AKVHGGLDGA
  51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
 101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

```

              10      20      30      40      50      60
m043.pep      MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF
              |||
a043           MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF
              10      20      30      40      50      60

              70      80      90      100     110     120
m043.pep      QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV
              |||
a043           QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV
              70      80      90      100     110     120

              130
m043.pep      VVAAEGEAQX
              |||
a043           VVAAEGEAQX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
  1 ATGCTGCCCG ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGCGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGCCC TTCGATAACG GCGGTCAGCT
 201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
 251 CGGCTGCCGT AGCGCATTA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
  1 MLPDQSVEFL PQVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
  51 GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
  1 ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGTCC TTCGATGACG GCAGTCAGTT
 201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
 251 TGGCTACCGT AGCGCAyTAa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
  1 MPSDXSVEFF PEVVFDGLF GGGFPAVALP TVYPVFHAI F DVLRVGADDD
  51 GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
  1 GTGCCGTCGG ACCAGCGCGT CGAGTCTTTT CCACAAGTCG TCGTTTTTGA
 51 CGGGCTGTTT GCGGCGCGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTCAGTCC TTCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGCTGCCGT AGCGCATTA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
  1 VPSDQREFF PQVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
 51 GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

```

      10      20      30      40      50      60
m044.pep  MPSDXSVEFFPEVVFDGLFGGGFAVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS
          :||| :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a044      VPSDQREFFPQVVFDGLFGGGFAVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQS
          10      20      30      40      50      60

      70      80      90
m044.pep  FDDGSQFHAVVGGLRFAAEKFFFVATVAHX
          |||:||||:||||:||||:||||:||||:
a044      FDDGGQFHTVVGGLRFAAEKFFFVAVAHX
          70      80      90
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

```
m044/g044

      10      20      30      40      50      60
m044.pep  MPSDXSVEFFPEVVFDGLFGGGFAVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS
          | | |||:|:||||:||||:||||:||||:||||:||||:||||:||||:
g044      MLPDQSVEFLPQVVFDGLFGGGFAVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQP
          10      20      30      40      50      60

      70      80      90
m044.pep  FDDGSQFHAVVGGLRFAAEKFFFVATVAHX
          ||:|:|:||||:||||:||||:|:||||
g044      FDNGGQLHAVVGGLRFAAEKFFFAAFAHX
          70      80      90
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
  1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGcgcc gCGCCTGTAT
 51 GATGACCATC CGCACGCGGT CGTCTGCAA ACGTAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCGGGG
151 CTGATGGTTT CGGTTATGCC gaATATGGAA AGGCTGCCGt TTTcGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGagaGCGCG AGcagcaagt cggcatcttC
351 CgcgccggcG Cgttataatg tgAAGGGGGA TGCgcggttg ccgaAAACGG
401 TTTGGacatc gaggcggtcg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcg9 TTACGTCGTT GTTGGTGATG GCGGCAAGGT TTTGCGCGAC
```

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501 GGTAGAACCT ACCTGCCCCGT TGCCTAAAAT GAGGATTTTC ACGGTATGGG
 551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep
 1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
 51 LMVSVMPNME RLPFSLFSSL GLRYSRYSL RTRAMRPGML NRSAATLQAT
 101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM
 151 SITVTSLLVM AARFCATVEP TCPLPKMRIF TVWVAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq
 1 ATGTCGGCAA TGCTGCGTCC GACAAGCAst CCGC.r.sGC gCGcCTGTAT
 51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
 101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
 151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
 201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
 251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
 301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
 351 CGCGCCGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
 401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
 451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
 501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
 551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep
 1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
 51 LMVSVMPNME RLPFSLFSSL GLRYSRYSL RTRAMRPGML NRSAATLQAT
 101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
 151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq
 1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT
 51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
 101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
 151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
 201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
 251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
 301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
 351 CGCGCCGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
 401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
 451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
 501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
 551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep
 1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
 51 LMVSVMPNME RLPFSLFSSL GLRYSRYSL RTRAMRPGML NRSAATLQAT
 101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
 151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSXPXXRACMMTI	IRTRSSAKRKT	CNAPGQSIRP	PASCSVTSCSGL	LMVSVMPNME	
a046	MSAMLRPTSSPPRRACMMTI	IRTRSSAKRKT	CNAPGQSIRP	PASCSVTSCSGL	LMVSVMPNME	

245

	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKTGNAPGQSIRPASC SVTSCSGLMVSVMPNME					
g046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKTGNAPGQSIRPASC SVTSCSGLMVSVMPNME					
	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

```

1  ATGGTCATCA TACAGGCGcg gcGCGGCGGG CTGCTTGTCG GACGCAGCAT
51  TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCCTCATC
151 ATCGAAGGCG ACGAAATCCT GTTTGCCGCC GCCGCCGAAA ACATCGGGGC
201 GGTCATACCc gaATTGCGCC CCAAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGCGCG CGGCAACATc tgctACCGCC TCGCCAAGCA GCTCGAACAC

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301 GCATAcacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAAC ctcgAcaaCA CCCTCGTCCT GCAAGGTTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTAtg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcggtca tcggCATCGT CAACCGCTCA AGCTACGTCTG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGAGAAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1 MVIIQARRGG LLVGRSIADI AQDLPDGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLEDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS AIIGRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1 ATGGTCATCA TACAGgCGcG C..syGCGGA sTGCTTGTCTG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGCGCG
201 GGTCATACCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGGCGGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTGAACACG CATACAACGT yAAAATCATC GAATGCCGGC CGCGCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTTCGG
401 CAACCGACGA AACCTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GCGGaaAAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCGTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGCGACAT
651 CGTTGCCGTC CACCCCATCC GGCGCGGCAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAGC
751 GGATCAAAT GGCCCGAAGG CTGCCACATT GCCGCCGTCG TCCGCGCCGG
801 AACCGGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTC GTCTCGCGCC GGCGCATCCT GAACGAACTG
901 GAAAACTCA TCCAGGTCAA AATGGGCTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1 MVIIQARXXG XLVGRSIADI AQDLPDGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV LQGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE AIEVVAHGDKK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRRILNEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1 ATGGTCATCA TACAGGCGCG GCGCGGCGGA CTGCTTGTCTG GACGCAGCAT

```

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```
51  TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTACATACC GAATTGCGCC CCAAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGGCGG CGGCAACATC GGCTACCGTC TCGCCAAGCA GCTCGAACAC
301 GCATACAACG TCAAAATCAT CGAATGCCGG CCGCGCCGTG CCGAATGGAT
351 AGCCGAAAAC CTCGACAACA CCCTCGTCCT GCAAGGTTCT GCAACCGACG
401 AAACCCTGCT CGACAACGAA TACATCGACG AAATCGACGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTATG TCCGCCCTTT TGGCGAAAAA
501 CCTCGGCGCG AAGCGCGTCA TCGGCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCACACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGCGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGA AAAA ACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA
```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```
a047.pep
1  MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51  IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI GYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCA
151 LTNDDES NIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS A IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*
```

m047/a047 96.5% identity over a 312 aa overlap

```

      10      20      30      40      50      60
m047.pep  MVIIQARXXGXLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA
          ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA
          10      20      30      40      50      60

      70      80      90     100     110     120
m047.pep  AAENIGAVIPELRPKETQRNPXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
          ||||| : || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      AAENIGAVIPELRPKETSTRR---IMIAGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
          70      80      90     100     110

      130     140     150     160     170     180
m047.pep  AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV
          120     130     140     150     160     170

      190     200     210     220     230     240
m047.pep  NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
          180     190     200     210     220     230

      250     260     270     280     290     300
m047.pep  TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
          240     250     260     270     280     290

      310
m047.pep  EKLIQVKMGFFGX
          ||||| |||||
```

a047 EKLIQVKMGFFGX
 300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNQXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
g047	AAENIGAVIPELRPKETSTRR---IMIAGGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL	300
g047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL	297
m047.pep	EKLIQVKMGFFGX 313	
g047	EKLIQVKMGFFGX 310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

```

1   ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTTACCCG CCAAATGCTC
151 AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201 cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGGC ATACCTCGTG GCAAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCCG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351 TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

```

1   MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  KQTGLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAV YEFEVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

```

1   ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC GGCCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG

```

```
m048.pep
  1  MLNKGELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *
```

```
a048.seq
1  ATGCTCGACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCTGAT
51  TTA CTACGTC GGGCCCGTCG ATCCGGTCCG CGACGAAATC GTCGGCCCGAG
101 CAGGTC CGAC CACCGCCACC CGCATGGACA AATTCAACCG CCAATGCTC
151 GAACAAACCG ACCTCTTGGG CATGATCGGC AAATCCGAGC CGGGCGCGCG
201 CACCTGCGAA GCCATCGCCG ACAACAAAGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGCG GTATCTCGTG GCAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTC CCGG AATTGGGCAT GGAAGCCATT TACGAATTTC AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCGG TAGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCC CCAATGGCAG GCGAAAATCG GCATCATCCC CGTCAAATCT
451 TGA
```

```
a048.pep
1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
51  EQTDLLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 APFELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPPQWQ AKIGIIPVKS
151 *
```

	10	20	30	40	50	60
m048.pep	MLNKGEE	LPVDF	TNRLI	YYVGP	VPDVG	DEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG
	:			:		
a048	MLDKGEE	LPVDF	TNRLI	YYVGP	VPDVG	DEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIG
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVAT	CEAIAD	NKAVYL	MAVGG	AAYLV	AKAIKSSKVLAFPELGMEAIYEFVVKDMPV
	:					
a048	KSERGAAT	CEAIAD	NKAVYL	MAVGG	AAYLV	AKAIKSSKVLAFPELGMEAIYEFVVKDMPV
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSK	GESIHA	TAPRK	WQAKI	GIIIP	VESX
				:		
a048	TVAVDSK	GESIHA	TAPPQ	WQAKI	GIIIP	VKSX
	130	140	150			

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

250

m048/g048

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	:					
g048	MLDKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLKQTGLLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPV					
	:					
g048	KSERGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
g048	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

g049.seq

1	ATGCGGGCGC	AGGCGTTTGA	TCAACCGTTC	GGTCAGCTCC	TGTTCCGACA
51	GGCAGAACAC	TTCGCGCCCG	TTGACGGCTT	TCGGGTTTCAG	GATATTGATT
101	TGGACGGGCA	TCAACGCCTC	TTCCGCACCG	CCTTCGCCGT	TTTCCGCAAC
151	CCCGTCTGCC	GCCGTACCGG	ATTCTGCCGC	ATCGGCGTTT	TCCCCGCCCT
201	CAATCTGTGC	GGTTTCAAAT	TCGGCACTGT	CTTTTGTGGC	ATCGAACCGG
251	ATTCTCCGCC	GCGATTTCGAT	GTGTTTTTCC	GAAAccggca	tTTGCAGGGA
301	AGCCTgcgcg	TTGAGCCAGT	TTTCCTGAAG	GACGATCATC	GGGTCGGTTT
351	CGACTTCCTC	GCCGCAATCG	GCAACGGCgc	tGTTGTGTTC	TTCTGCCAT
401	TTCTTCAGAT	ACGCCTTAA			

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

g049.pep

1	MRAQAFDQPF	GQLLFGQAEH	FAPVDGFRVQ	DIDLGHQRL	FRTAFVFRN
51	PVCRRTGFCR	IGVFPAFNLC	GFKFGTVFFG	IEPDSPPRFD	VFFRNRLQG
101	SLRVEPVFLK	DDHRVGDFDL	AAIGNGAVVF	FLPFLQIRL*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

m049.seq (partial)

1	ATGCGGGCGC	AGGCGTTTGA	TCAGCCGTTC	GGTCAGCTCC	TGTTCCGACA
51	GGCAGAACAC	TTCGCGCCCG	TTGACGGCTT	TCGGGTTTCAG	GATATTGATT
101	TGGACGGGCA	TCAACGTTTC	TTCCGCATCG	TTTTCCCCGT	TTTCCGAAAC
151	CGCCGGCTCA	TTCGTGCCCG	ATTCTGCCTC	GTCGGCGTTT	TCCCCGCTTT
201	CAATCTGTCC	GGTTTCAAAT	TCGACACTGT	CTTTTTTGGT	ATCAAACCGG
251	ATTCTCCGCC	GCGATTTCGAT	GTGTTTTTCC	GAAACCGACA	TTTGCAGGGA
301	AGCCTGCGCG	TTGAGCCAGT	TTTCCTGAAG	GACGATCATC	GGGTCGGTTT
351	CGACTTCCTC	GCCGCAATCG	GCAACGGCGG	CATTGTGTTC	CTCCTGCCAT
401	TTTTTCAGAT	ACGCCTT...			

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

m049.pep (partial)

1	MRAQAFDQPF	GQLLFGQAEH	FAPVDGFRVQ	DIDLGHQRF	FRIVFPVFRN
51	RRLIRAGFCL	VGVFPAFNLS	GFKFDTVFFG	IKPDSPPRFD	VFFRNRLQG
101	SLRVEPVFLK	DDHRVGDFDL	AAIGNGGIVF	LLPFLQIRL...	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 209>:

a049.seq

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```

1   ATGCGGGCGC AGGCGTTTGA TCAGCCGTTT GGTGAGCTCC TGTTCCGACA
51  GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTCAG AATATTGATT
101 TGGACGGGCA TCAACGCTTC TTCCGCACCG CCTTCGCCGT TTTCCGCAAC
151 CCCGTCTGCC GCCGTACCCG ATTCTGCCGC ATCGGCGTTT TCCCCGCCTT
201 CAATCTGTCC GGTTCCTAAAT TCGGCACTGT CTTTTTTGGC ATCAAACCGG
251 ATTCTCCGCC GCGATTGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT

```

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

```

a049.pep
1   MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFAVERN
51  PVCRRTRFCR IGVFFAFNLS GFKFGTVFFG IKPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGFDL AAIGNGGIVF LLPFFQIRL

```

m049/a049 90.6% identity over a 139 aa overlap

```

              10      20      30      40      50      60
m049.pep      MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLGDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||:|||||:|||||:|||||:|||||:|||||
a049           MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLGDGHQRFRTAFAVERNPVCRRTRFCR
              10      20      30      40      50      60

              70      80      90      100     110     120
m049.pep      VGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              :|||||:|||||:|||||:|||||:|||||:|||||
a049           IGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              70      80      90      100     110     120

              130     139
m049.pep      AAIGNGGIVFLLPFFQIRL
              |||||:|||||
a049           AAIGNGGIVFLLPFFQIRL
              130

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

```

m049/g049
              10      20      30      40      50      60
m049.pep      MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLGDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||:|||||:|||||:|||||:|||||:|||||
g049           MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLGDGHQRLFRTAFAVERNPVCRRTGFCR
              10      20      30      40      50      60

              70      80      90      100     110     120
m049.pep      VGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              :|||||:|||||:|||||:|||||:|||||:|||||
g049           IGVFFAFNLSGFKFDTVFFGIEPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              70      80      90      100     110     120

              130     139
m049.pep      AAIGNGGIVFLLPFFQIRL
              |||||:|||||
g049           AAIGNGAVVFFLPFLQIRLX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

```
g050.seq
1  atgggCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  cacgcccGAA AAAGccgtgt TGATGGcaaa AGAATCCCTG ATGAGCCACA
101 TCGAcatCca aGaATTGCAG GAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGGtcc
351 TGTCGAactc acgccGCcgc gtgtCGAAGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

```
g050.pep
1  MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

```
m050.seq
1  ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
51  C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA TGGCCCCATT TGA
```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

```
m050.pep
1  MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

```
a050.seq
1  ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  TACGCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA CTGGCCC
```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

```
a050.pep
1  MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP
```

m050/a050 97.7% identity over a 129 aa overlap

```

10      20      30      40      50      60
m050.pep  MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
|||||
a050      MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
```

253

	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
a050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
g050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACAACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGGAAGGCAA CACCCTGCGC GCTTCCTCC TCGCCGATCC
351 GGCCGCGCAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAATC CAAACTCGCT ATGCTCAACC CTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGGT
551 GTCTCCCGG CATCTGGGC ATCGGCATCG GCGGCACgC CGAAAAAGCC
601 GTGTTGATGG cgaAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GTCCTGTCGA ACTCACGCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCCG ACAACGGCAA
951 ACGGTCGAT GTCGATAAGC TGACCAAAGA AGAAGTGGA AGCTGGAAAA
1001 CCGCGACGAT ATTGCTGTTG AACGGCAAAA TCCTCACC GGCGCATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGGCGAGG AGTTGCCCGT
1101 CGATTTACAC AACCCGCTGA TTTACTACGT CGGCCCGT GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAAATGCT CAAACAAACC GGCCTCTTGG GCATGATCGG

```

```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGACCT CATGGCAGTC GGCGGCGCGG CATACTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCC GAATGGGTA TGGAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCCG AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGC GCAAATGGCA GCGGAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVGMDVQWDADMSV EKMVNEGVR
101 AYTWEENTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQG
251 LGLLTTVLVDV KILDYPHTAA SKPIAMIPNC AATRHVEFEL DSGGPVELTP
301 PRVED*PDLT YSPDNKGRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVNMMLD KGEELPVDFN NRIYYVGPV DPGDEVVGP AGPTTATRMD
401 KFTROMLKQT GLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAVYEF EVKDMPVTVA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11 QSIDAFQFISYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
      Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53 QAFHDASFMLRPAHQKQVAAIILHDEPEASEND---KYVALQFLRNSEIAAKGVLPCTQDTG 109

```

```

Query: 71 IATVFLKVGMDVQWDADMSVEKMVNEGVRRAAYTWEENTLRASVLADPAGKRQNTKDNTPA 130
      A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAIIVGKKGQVR-WTGGGD-EETLSKGVNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCAAKGGGSENKSKL-----AMLNPSDNIVDWVLKTIPTMGAGWCP 185
      I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGDYKFLCVAKGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAACP 225

```

```

Query: 186 PXXXXXXXXXTPEKAVLMAKESLSHIDIQELQEKAAASGAELSTTEALRLELFEKVNXXX 245
      P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGTSATNLKTVKLASAHY-YDELPTGEGNEHQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXXTVDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSG----PVELTTP 301
      D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSADRNIAKINREGIWIEKLEHNPG 343

```

```

Query: 302 RVEDXPDLTYSPDNKGRVDVDKLTKE---EVASWKTGDVLLNGKILTGRDAAHKRLVNM 358
      + +VD+++ KE +++ + L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRLSLTGTIIVGRDIAHAKLKL 403

```

```

Query: 359 LDKGEELPVDFNRLIYXXXXXXXXXXXXXXXXTTATRMDKFTROMLKQTGLLGMIGK 418
      +D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSIMMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVAVGG-AAYLVAKAIKSSKVLAFPGLGMEAVYEFVVDMPV 477
      R +A + YL ++GG AA L ++IK + +A+PELGMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSIIGGPAVLAQQSIKHLECVAYPELGMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
      + VD KG
Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGCGA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACAACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

```

```

301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGGCAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCATA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAATC CAAACTCGCC ATGCTCAATC CTTCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGCTGATGG CAAAGAGTC CCGATGAGC CACATCGACA TTCAAGAATT
651 GCAGGAAAAG GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTTGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTGCA ATTTGAATTG GACGGCTCAG GCCCTGTGCA ACTACGCCG
901 CCGCGCTCG AAGACTGGCC CGATTTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGGCA AGCTGAAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTACAC AACCGCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCC
1151 GCGATGAAGT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAACCC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTGCGA AGCCATCGCC GACAACAAAG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCGCC GAATTGGGCA TGGAAAGCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGCG GCAAATGGCA GCGGAAAATC
1501 GGCATCATCC CCGTCGAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVM NVQWDADMSV EEMVNEGVRR
101 AYTWEANTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELF EK VNALGIGA QG
251 LGGLTTVLDV KILDYPTHA SKPIAMIPNC AATRHVEFEL DGSGPVLT P
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTRDA
351 AHKRLVDM LN KGEELPVDF T NRIIYVGPV DPGVDEVVGP AGPTTATRMD
401 KFTRQMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLM AV GGAAYLVAKA
451 IKSSKVLAF P ELGMEAIYEF EVKDMPTVTA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*

```

m050-1/g050-1 98.2% identity in 507 aa overlap

	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
g050-1	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050-1.pep	NNRPICQDTGIATVFLKVMNVQWDADMSVEEMVNEGVRRAYTWEGNTLRASVLADPAGK					
g050-1	NNRPICQDTGIATVFLKVMNVQWDADMSVEEMVNEGVRRAYTWEGNTLRASVLADPAGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m050-1.pep	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG					
g050-1	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m050-1.pep	AGWCPPGILGIGIGGTPEKAVLMKESLMSHIDIQELQEKAAASGAELSTTEALRLELF EK					
g050-1	AGWCPPGILGIGIGGTPEKAVLMKESLMSHIDIQELQEKAAASGAELSTTEALRLELF EK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m050-1.pep	VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVLT P					
g050-1	VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVLT P					
	250	260	270	280	290	300

256

	310	320	330	340	350	360
m050-1.pep	PRVEDWPDLT	YSPDNGKRVD	VDKLTKEEVASWKT	GDVLLNGKILTGRDA	AAHKRLVDMLN	
g050-1	PRVEDXPDLT	YSPDNGKRVD	VDKLTKEEVASWKT	GDVLLNGKILTGRDA	AAHKRLVNMLD	
	310	320	330	340	350	360
	370	380	390	400	410	420
m050-1.pep	KGEELPVDF	TNRLIYYVGP	VPVGVGPA	GPTTATRMDK	FTROMLEQ	TDLGMI
g050-1	KGEELPVDF	TNRLIYYVGP	VPVGVGPA	GPTTATRMDK	FTROMLKQ	TGLLGM
	370	380	390	400	410	420
	430	440	450	460	470	480
m050-1.pep	RGVATCEAI	ADNKAVYILMA	VGGAAAYLVA	KAISKSVLAF	PELGMEAI	YEFV
g050-1	RGAATCEAI	ADNKAVYILMA	VGGAAAYLVA	KAISKSVLAF	PELGMEAV	YEFV
	430	440	450	460	470	480
	490	500				
m050-1.pep	VDSKGESI	HATAPRKWQAK	IGIIPVESX			
g050-1	VDSKGESI	HATAPRKWQAK	IGIIPVESX			
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

a050-1.seq

1	ATGACCGTCA	TCAAACAGGA	AGACTTTATC	CAAAGCATT	GCGATGCCTT
51	CCAATTTCATC	AGCTACTACC	ATCCCAAAGA	CTACATCGAC	GCGCTTTATA
101	AGGCGTGGCA	GAAGGAAGAA	AACCCCGCCG	CCAAAGACGC	GATGACGCAG
151	ATTTTGGTCA	ACAGCCGCAT	GTGTGCCGAA	AACAACCGCC	CCATCTGCCA
201	AGATACCGGT	ATCGCGACCG	TGTTTTTGAA	AGTCGGTATG	GATGTGCAAT
251	GGGATGCAGA	CATGAGCGTC	GAAGAGATGG	TTAACGAAGG	CGTGCGCCGC
301	GCCTACACTT	GGGAAGGCAA	TACGCTGCGC	GCTTCCGTTT	TCGCCGACCC
351	CGCCGGCAAA	CGCCAAAATA	CCAAAGACAA	CACGCCCGCC	GTCATCCATA
401	TGAGCATCGT	GCCGGGCGAC	AAAGTCGAAG	TAACCTGCGC	GGCAAAAGGC
451	GGCGGTTCCT	AAAACAAATC	CAAACCTGCC	ATGCTCAACC	CTTCCGACAA
501	CATCGTTCAT	TGGGTATTGA	AAACCATTC	GACCATGGGC	GCGGGCTGGT
551	TCCTCCCGG	CATCTTGGGC	ATCGGCATCG	GCGGTACGCC	CGAAAAAGCC
601	GTGTGATGG	CGAAGAAATC	CCTGATGAGC	CACATCGACA	TCCAAGAATT
651	GCAGGAAAAA	GCCGCGTCCG	GCGCGGAATT	GTCCACCACC	GAAGCCCTGC
701	GCCTCGAACT	CTTTGAAAAA	GTCAACGCGC	TAGGCATCGG	CGCGCAAGGC
751	TTGGGCGGTC	TGACCACCGT	GTGGACGTG	AAAATCCTCG	ATTACCCGAC
801	CCACGCGGCC	TCCAAACCGA	TTGCCATGAT	TCCGAACCTG	GCCGCCACCC
851	GCCACGTCTG	ATTGAATTG	GACGGCTCAG	GCCCTGTCTG	ACTCACGCGG
901	CCGCGCGTCG	AAGACTGGCC	CGATTTGACT	TACAGCCCCG	ACAACGGCAA
951	ACGCGTCGAT	GTCGACAAGC	TGACCAAGA	AGAAGTGGCA	AGCTGGAAAA
1001	CCGCGGACGT	ATTGCTGTTG	AACGGCAAAA	TCCTACCCGG	CCGCGATGCC
1051	GCACACAAAC	GCCTCGTCGA	TATGCTCGAC	AAAGGCGAAG	AATTGCCCGT
1101	CGATTTCACC	AACCGCCTGA	TTACTACGT	CGGCCCCGTC	GATCCGGTCG
1151	GCGACGAAAT	CGTCGGCCCA	GCAGGTCGGA	CCACCGCCAC	CCGCATGGAC
1201	AAATTCAACC	GCCAAATGCT	CGAACAACCC	GACCTCTTGG	GCATGATCGG
1251	CAATCCGAG	CGCGGCGCGG	CCACCTGCGA	AGCCATCGCC	GACAACAAAG
1301	CCGTGTACCT	CATGGCAGTC	GGCGGCGCGG	CGTATCTCGT	GGCAAAAGCC
1351	ATCAAATCTT	CCAAAGTCTT	GGCGTTCCCC	GAATTGGGCA	TGGAAGCCAT
1401	TTACGAATTT	GAAGTCAAAG	ACATGCCCGT	AACCGTCGCC	GTAGACAGCA
1451	AAGGCGAATC	CATCCACGCC	ACCGCCCCGC	CCCAATGGCA	GGCGAAAATC
1501	GGCATCATCC	CCGTCAAATC	TTGA		

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

a050-1.pep

1	MTVIKQEDFI	QSICDAFOFI	SYYHPKDYID	ALYKAWQKEE	NPAAKDAMTQ
51	ILVNSRMCAE	NNRPICQDTG	IATVFLKVGM	DVQWDADMSV	EEMVNEGVR
101	AYTWEGNLT	ASVLADPAGK	RQNTKDNTFA	VIHMSIVPGD	KVEVTCAAKG
151	GSSENKSKLA	MLNPSDNIVD	WVLKTIPTMG	AGWCPPGILG	IGIGGTPEKA
201	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLLEFEK	VNALGIGAOG
251	LGLLTTLVDV	KILDYPTTHA	SKPIAMIPNC	AATRHVEFEL	DGSGPVLETP
301	PRVEDWPDLT	YSPDNGKRVD	VDKLTKEEVA	SWKTGDVLLL	NGKILTGRDA
351	AHKRLVDMLD	KGEELPVDF	TNRLIYYVGP	VPVGVGPA	GPTTATRMD
401	KFTROMLEQT	DLGMIKSE	RGAATCEAIA	DNKAVYILMA	VGGAAAYLVA
451	IKSSKVLAF	ELGMEAIYEF	EVKDMPVTVA	VDSKGESIHA	TAPPQWQAKI
501	GIIPVKS*				

a050-1/m050-1 98.4% identity in 507 aa overlap

	10	20	30	40	50	60
a050-1.pep	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
m050-1	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
a050-1.pep	70	80	90	100	110	120
m050-1	NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTRASVLADPAGK					
	70	80	90	100	110	120
a050-1.pep	130	140	150	160	170	180
m050-1	RQNTKDNTPAVIHMSIVPGDKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG					
	130	140	150	160	170	180
a050-1.pep	190	200	210	220	230	240
m050-1	AGWCPPGILGIGIGGTPEKAVLMKESLMSHIDIQELQEKAASGAELSTTEALRLELFEK					
	190	200	210	220	230	240
a050-1.pep	250	260	270	280	290	300
m050-1	VNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGS GPVELTP					
	250	260	270	280	290	300
a050-1.pep	310	320	330	340	350	360
m050-1	PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD					
	310	320	330	340	350	360
a050-1.pep	370	380	390	400	410	420
m050-1	KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE					
	370	380	390	400	410	420
a050-1.pep	430	440	450	460	470	480
m050-1	RGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFV KDMPTVA					
	430	440	450	460	470	480
a050-1.pep	490	500				
m050-1	VDSKGESIHATAPPQWQAKIGIIPVKSX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

```

g052.seq
1  ATGGCTTTGG TGGCGGAGGA AACGAAAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGCGGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGGG CTA CTCCGA
251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTGCGCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep

```

      1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
    51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
   101 RLRLETTWSP ACRKVKNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

```

m052.seq
      1 ATGGCTTTGG TGGCGGAGGA AACGGAATA TCCGCGCCGT GTTCAAAGG
     51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
    101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
    151 AAGGGGTGG ACGGCGTTTC CAAAACAGC AGTTTGGTGT TGGCTTTGAC
    201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGGG CTACTCCGA
    251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
    301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
    351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

```

m052.pep
      1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
     51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
    101 RLRLETTWSP ACRKVKNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

```

a052.seq
      1 ATGGCTTTGG TCGCGGAGGA AACGGAATA TCCGCGCCGT GTTCAAAGG
     51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
    101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
    151 AAGGGATTGG ACGGCGTTTC CAAAACAGC AGTTTGGTGT TGGCTTTGAC
    201 GGCGGCTTTC CATTGTTTA TATCAGTCGG CGACACGTGA CTCATTCTGA
    251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
    301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA
    351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

```

a052.pep
      1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
     51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPLVTM LLIKPTVVPN
    101 RLRLEITWSP ACKKVKNA*

```

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEISAPCFKGXEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTAAFHSFISVGDXTLTPMPNLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

```

m052/g052
      10      20      30      40      50      60
m052.pep MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS
          |||||

```


259

```

g052      MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANSASAKASKSATSPKGLDGVSKNS
              10      20      30      40      50      60

              70      80      90      100     110     120
m052.pep   SLVLALTAAFHSFISVGDTWLTSMPLATMLLIKPTVVPNRLRLEITWSPACKVKVNAAX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g052      SLVLALTAAFHSFISVGDTRLTPMPLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
  1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
 51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101  AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151  AGTCCGGGGC GGatacCGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201  GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251  TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301  GCGACTTCAA AACCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351  AAGCTCCGCC TCGGGATGGT CGGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
  1  MCMPYAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
 51  SPGRIPAASF SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101  ATSKPMTMPP PFCCLRISSA CGWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
  1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
 51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101  TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151  CGGATGTTGG CCGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201  TGTCCACGGG TGGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251  GGGAAAAGAG TTCCACGCCG TCCACAACCT TCCACGCCGC TTCTTGATCG
301  GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351  AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
  1  MCMPYKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
 51  RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASXS
101  ATSKPMTMPP PFCCLRISAA XGWSNPNV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
  1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
 51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101  AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151  AATCCGGGGC GGATGTTGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201  GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251  TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301  GCTTGGTCGG CCACTTCAA GCCGATGACG ATGCCGCCGC CGTTTTGCTG
351  TTTGCGGATA AGTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
  1  TCMSYKIRVS DGICGVFPPM PSEXRNQRAS ACFKSSIKSP TYSKPTDRRT
 51  NPGRMLAASF SSGCILPCVV VHGWVVERT SPRLAVREKS STPSTTFHAA
101  AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEXRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCLRI				
a073	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAAAWSATSKPMTMPPPFCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNPNVX				
a073	SSAXGWSGNPNVX				
	130				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
g073	MCMPIAIRVSDGICRIFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAAAF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCLRI				
g073	SSGCILPCVVVHGLVMVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNPNVX				
g073	SSACGWSGNPNVX				
	120				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAATA CAAAAAGCGC
51  GCGCAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCCGTTTCGG GCAACGCTGC GTTTGCCTGT
151 GCCGCCAAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTAGAGA CCGCTGCGG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAA ATTACAAATT
351 CCCCCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTT ATAGCTGTCA
401 TATTTACCGG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFITLLT MENTKSAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLQ VLINFMIFS TKFLKKVCV LCEGFRDLRP
101 GLLNLIFFV ESENYKPAY LFQCRKSVF IAVIFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 237>:

```
m075.seq
1   ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCGAAAATG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCCGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTCATGAT ATTTTCCTTC AAAAAGTGTT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 238; ORF 075>:

```
m075.pep
1   MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLRL VLINFMIFSF KKCLAVMDGA FFRRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

```
m075/g075

      10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          ||||||||||||||| ||||||||||||||| : ||||||| |||||
g075      MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAAVT
          10      20      30      40      50      60

      70      80      90      100     110
m075.pep  TASFAPYLRLQLINFMIFSF----KKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVAD
          ||||||||||||||| |||: : :| |::: :| |::: :|
g075      TASFAPYLRLQLINFMIFSFTKFLKKVCGLCEGFRDRLPGLNLNLIFFVESENYKFPAY
          70      80      90      100     110     120

      120     130
m075.pep  FFQTCVNRFFEVEIIGIGDX
          :|| :| :| :|
g075      LFQCRAKSVFIAVIFTGX
          130
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 239>:

```
a075.seq
1   ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAAGA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCTGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTCATGAT ATTTTCCTTC AAAAAGTGTT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 240; ORF 075.a>:

```
a075.pep
1   MPSYFITLLT MEKTKSAAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLRL VLINFMIFSF KKCLAVMDGA FFRRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m075.pep	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
	130					
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

```

g080.seq
1   ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAAGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA TACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGGTTGCA CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAA TGTCGTTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACgaGA TGAAACGCCT CCgGCTTTT
601 ACcgAAGCGT GGCAGCATCT gttgcGTAAG AATAAAAATC GGTtATCCTA
651 TGTGGATATG Aggtataagg acggatttTC agtcccccat gctCCCACG
701 GTTTACCCGA AAAAGAATcc gAAGAAAtt gggAACaggt ttgggacata
751 ttacggcctg gcgtcggaaa cggttcgacg caaatttcaa tcagttatAA
801 GGGCAGacga acaatggaac AGcagtaa
  
```

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

```

g080.pep
1   MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
51  SDKKALGSLA KEYIYHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSAWNVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVPH APDGLPEKES EEWYEQVWDI
251 LRPGVGNGST QISISYKGRR TMEQQ*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

```

m080.seq
1   ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGACATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGGTCGCG CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
  
```

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep

1 MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
 51 SDKKTLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

	10	20	30	40	50	60
m080.pep	MWDNAEAMERL LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY SDKKTLGSLA					
080	MWDNAEAMERL LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY SDKKALGSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILRTDINGAQEAY RRYPWIASVM VRRRFPDVEVVLTERKPVARWGDHALVDG					
080	KEYIHGNILRTDINGAQEAY RRYPWIASVM VRRRFPDVEVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLDRPGMPVFRGA EGTSAEMLRRYDEFSTVLAK QGLGIKEMTYTARSAWIVVL					
080	EGNVFEARLDRPGMPVFRGA EGTSAEMLRRYDEFSTVLAK QGLGIKEMTYTARSANVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGRENEMKRLRLFTEAQHLLRK NKNRLSYVDMRYKDGFSVRY ASDGLPEKES					
080	DNGITVRLGRENEMKRLRLFTEAQHLLRK NKNRLSYVDMRYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
080	EEYWEQVWDILRPGVGNSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq

1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
 101 CGAATCATCT GCCCGTCAAG CAGGTGTGCG TGAAGGGCAA CCTAGTTTAT
 151 TCCGATAAGA AAGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGTATC
 251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTCCCGA CACGGTTGAG
 301 GTCGTCCTGA CCGAGCGCAA GCCGTCGCG CGTTGGGGCG ACCATGCCTT
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGGAC AGACCCGGAA
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
 451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTTG GACAACGGCA

264

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551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAAATC GGTTATCCTA
651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCGACG
701 GTTTACCCGA AAAAGAATCC GAAGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

```

1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYN SNHLPVK QVSLKGNLVY
51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRY PWIASVM VRRRFPDVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA EG TSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARS AWIVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK KNRLSYVDM RYKDGFSVRY APDGLPEKES EE*

```

m080/a080 99.2% identity over a 242 aa overlap

m080.pep	10	20	30	40	50	60
	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLFPVKQVSLKGNLVYSDKKTGLGSLA					
a080	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLFPVKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDVEVVLTERKPVARWGDHALVDG					
a080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDVEVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLDRPGMPVFRGAEG TSAEMLRRYDEFSTVLAKQGLGIKEMTYTARS AWIVVL					
a080	EGNVFEARLDRPGMPVFRGAEG TSAEMLRRYDEFSTVLAKQGLGIKEMTYTARS AWIVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
a080	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
101 TTCGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GCGCGGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
301 CCGTTTGTGT TCGGCATTAC CGGTTCTGGG GCAAGACGA CGGTGAAGGA
351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCATGAT GCCGTTTCGG
401 CGACGGCAGG CAACTTCAAC AACCACAtcg gaTTGCCGCT GACTTTATTG
451 AAATtaaAcg aAAAAACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTTGGcgaa ctggcggTt taacgcaaaT CGCCAAACCC GATGCCGCTT
551 TGGtcaACAA CGCCTGCGC GCCCATGTCG GATGCGGTTt cgacggagtg
601 GGCATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTcAGA
651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGTT TAATTGAAT ACGTGCACCT TCGGCGTCGA TAGCGGCGAT
751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT

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265

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801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCCGCCG CATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGAGCC ACGATTTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGAtggAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

g081.pep

```

1 MKPLDLNFIC QALKLPMPSE NKPVSRIVTD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTQIAKP DAALVNNALR AHVGCDFDGV
201 GDIKAKSEI YAGLCSDGMA LIPOEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNVHNAA AAAALALAAG
301 LSLNDVAEGL QGFSNIKGRL NVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMGELGED EAAAMHAEVG AYARDQIEA AYFVGDNVSE
401 AAKEFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

m081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCGTAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGCGCG CGGTTGTGGT
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTCGGGCG GCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCgCCGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AAGTTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGCGGAA CTGGCGGTTT TAACGCAmAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTCAGA
651 CGGCATTGCA CTGATTCTCT AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCG CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCGCCGC
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTTGCCC GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTTC CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

m081.pep

```

1 MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTXIAKP NAALVNNAMR AHVGCDFDGV

```

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201  GDIKAKSEI YQGLCSDGIA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251  VHAENIVLKP LSCEFDLVCG DERAADVLPV PGRHNVHNAA AAAALALAAG
301  LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAIDVL
351  ARMPAPRIFV MGD MGELGEL GEDEAAAMHA EVGAYARDQG IEAAYFVGDN
401  SVEAAEKFGA DGLWFAAKDP LIQVLRHDL ERATVLVKGS RFMQMEEVVE
451  ALEDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng) from *N. gonorrhoeae*:

m081/g081

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSRDIRAGDVFFALAGERFDAHDFVEDVLAA					
	: : : : : :					
g081	MKPLDLNFICQALKLPMPSESKPVSRIVTDSRDIREGDVFFALAGGRFDAHDFVGGVLSA					
	10	20	30	40	50	60
m081.pep	70	80	90	100	110	120
	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	: : : : : :					
g081	GAAAVVVSREDCAALGGALKVDDTLAALQTLAKAWRDNVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	130	140	150	160	170	180
	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGEAVLTIXIAKP					
	: : : : : :					
g081	AVLRRRFGDDAVSATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGEAVLTQIAKP					
	130	140	150	160	170	180
m081.pep	190	200	210	220	230	240
	NAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSDGIALIPQEDANMAVFKTATLNLN					
	: : : : : : :					
g081	DAALVNNALRAHVGCDFGVGDIKAKSEIYAGLCSDGMALIPQEDANMAVFKTATFNLN					
	190	200	210	220	230	240
m081.pep	250	260	270	280	290	300
	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAADVLPVPGRHNVHNAAAAALALAAG					
	: : : : : :					
g081	TCTFGVDSGDVRAENIVLKPLSCEFDLVCGDERTAVVLPVPGRHNVHNAAAAALALAAG					
	250	260	270	280	290	300
m081.pep	310	320	330	340	350	360
	LSLNDVAEGLKGFSNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
	: : : : : :					
g081	LSLNDVAEGLQGFSNIKGR LNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
m081.pep	370	380	390	400	410	420
	MGDMGELGELGEDEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	: : : : : :					
g081	MGDMGELGE--DEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
m081.pep	430	440	450			
	LIQVLRHDLPERATVLVKGS RFMQMEEVVEALEDKX					
	: : : : :					
g081	LIQVLSHDLPERATVLVKGS RFMQMEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

a081.seq

```

1   ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGTG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTGC GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTCAGA
651 CGGCATGGCG CTGATTCCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTGATTTT
801 GGTGTGCGGC AACGAGTGCG CAGCCGTGGT TCTGCCCGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCCT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCCG CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

a081.pep

```

1   MKPLDLNFIC QALKLPMPSE SKPVSRIVD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNAMR AHVGCFGDGV
201 GDIAKAKSEI YQGLCSDGMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNAA AAAALSLAAG
301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

```

          10      20      30      40      50      60
m081.pep  MKPLDLNFICQALKLPMPSESKPVSRIVTDSDRDIRAGDVFFALAGERFDAHDFVEDVLAA
a081      MKPLDLNFICQALKLPMPSESKPVSRIVTDSDRDIRAGDVFFALAGGRFDAHDFVEDVLAA
          10      20      30      40      50      60

          70      80      90     100     110     120
m081.pep  GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA
a081      GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA
          70      80      90     100     110     120

          130     140     150     160     170     180
m081.pep  AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGEAVLTQIAKP
a081      AVLRRRFGDNAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGEAVLTQIAKP

```

268

	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVGC GFDGVGDI AKAKSEIYQGLCS DGIALIPQEDANMAVFKTATLNLN					
a081	DAALVNNAMRAHVGC GFDGVGDI AKAKSEIYQGLCS DGMALIPQEDANMAVFKTATLNLN					
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVVLVPVGRHNVHNA AAAAAALALAAG					
a081	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGNECAAVVLVPVGRHNVHNA AAAAAALSLAAG					
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	LSLNDVAEGLKGFSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEV GAYARDQGIEAAYFVG DNSVEAAEKFGADGLWFAAKDP					
a081	MGDMGELGE---DEAAAMHAEV GAYARDQGIEAAYFVG DNSVEAAEKFGADGLWFAAKDP					
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFMQMEEVVEALEDKX					
a081	LIQVLRHDLPERATVLVKGSRFMQMEEVVEALEDKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

```

g082.seq
1   aTGTGTTGT  TGAAGTTGCC  TGCCGTCGCC  GAAACGGCAT  CATCGCCGAA
51  ACGGCGGCGC  AATACCGCAG  CCAGCATCTC  CTTACCGTC  GTCTTGCCGC
101 CCGAACCGGT  AATGCCGAAC  ACAAACGGGT  TCACATTATC  GCGCCACGCC
151 TTCGCCAACG  TTTGCAACGC  GGCAAGCGTG  TCATCGACTT  TCAACGCGCC
201 GCCCAAAGCC  GCGCAATCTT  CGCGCGAAAC  CACAACCGCC  GCGCGCCCGC
251 CAGACAATAC  GCCTCCAACA  AAATCATGCG  CGTCAAACCG  CCCGCCCGCC
301 AATGCGAAAA  ACACATCGCC  TTCCCGAATA  TCGCGGCTGT  CGGTTACGAT
351 GCGCGACACG  GGTGTGTTTT  CAGACGGCAT  CGGAAGCTTG  AGGGCTTGGC
401 AGATGAAATT  TAGGTCCAGT  GGTTCATAT  TTGCTTTCGT  TAATATTCCG
451 GCGCGGACA  CATCGGTAGC  GGCTGATTT  TTTATCGCCT  GTTTTGCTGT
501 GGTAAAACAC  AGATTATTTT  CCCATTCTCA  TTCGGCATT  TTTCTGTACG
551 TATCATTTT  TAGACGTATT  TTAGCCGAT  TTGCCTTTTC  CCGCATACCA
601 CGGCGCGGG  TCGTCGGACT  GTCTGTCGAT  AAAGGCAAGG  TTATTGCCTT
651 CGCCCGGCAC  ATCGGGGACA  TTCCCCCAA  AATCATAGCC  GTCATCGGGC
701 AACTCGTCGG  TTTCGATACC  CGTCCAACG  CCGAATCCGC  GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

```

g082.pep
1   MWLLKLPAVA  ETASSPKRRR  NTAASISFTV  VLPPEPVMPN  TNGFTLSRHA
51  FANVCNAASV  SSTFNAPPKA  AQSSRETTA  AAPADNTPPT  KSCASNRPPA
101 NAKNTSPSRI  SRLSVTMRDT  GLFSDGIGSL  RAWQMKFRSS  GFIFAFVNIR
151 AADTSVAADF  FIACFAVVKH  RLFSHSHSAF  FLYVSFFRRI  FSRFAFSRIP
201 RRGVGLSVD  KGKVIAFARH  IGDIPPKIIA  VIGQLVGFD  RPTAESA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

```

m082.seq
1   ATGnnGTTGT  TGAAGTTGCC  TGCCGTCGCC  AACACGGCAT  CATCGCCGAA
51  ACGGCGGCGC  AATACCGCAG  CCAGCATTTC  CTTACCGTC  GTCTTGCCGC
101 CCGAACCGGT  AATGCCGAAC  ACAAACGGAT  TCACATTTTC  ACGCCACGCC
151 TTTGCCAGCG  TTTGCAATGC  GGCAAGCGTG  TCATCGACTT  TCAACGCGCC

```

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```

201 ATCCATTGCA GCACAAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGCC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGsATTT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CCGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
1  MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVM PN TNGFTFSRHA
51  FASVCNAASV SSTFNAPSIA AQSSRETTA AAPAANTSST KSCASNRSPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSDV KGKVIAFALH IGNIPPKIIA VIGQLVGFD T RPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

```

m082/g082

      10      20      30      40      50      60
m082.pep  MXLLKLPAVANTASSPKRRRNTAASISFTVVLPPEPVMPTNGFTFSRHAFASVCNAASV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       MWLLKLPAVAETASSPKRRRNTAASISFTVVLPPEPVMPTNGFTLSRHAFANVCNAASV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      10      20      30      40      50      60

      70      80      90     100     110     120
m082.pep  SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSPANAKNTSPARMSRLSVTMRDT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       SSTFNAPPKAAQSSRETTTAAAPADNTPPTKSCASNRPPANAKNTSPSRISRLSVTMRDT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      70      80      90     100     110     120

      130     140     150     160     170     180
m082.pep  GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF
          | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      130     140     150     160     170     180

      190     200     210     220     230     240
m082.pep  FLYVSFFRRIFSRFAFSRIPRRGVVGQSDVKGKVIAFALHIGNIPPKIIAVIGQLVGFD T
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGKVIAFARHIGDIPPKIIAVIGQLVGFD T
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      190     200     210     220     230     240

m082.pep  RPTAESAX
          | | | | | |
g082       RPTAESAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

```

a082.seq
1  ATGTGGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
51 ACGGCGGCGC AATACCGCAG CCAACATTC CTTCACCGTC GTCTTGCCGC

```

101	CCGAGCCGGT	AATACCGAAC	ACAAACGGGT	TCACATTCTC	GCGCCACGCC
151	TTCGCCAACA	TTTGCAACGC	GGTAAGCGTG	TCATCGACTT	TCAACGCGCC
201	ATCCATTGCA	ACGCAATCTT	CGCGCGAAAC	CACAAACGCT	CCCGCACCCG
251	CAGCCAATAC	GTCTTCAACA	AAATCATGCG	CATCAAACCG	CGCCCGCGCC
301	AATGCGAAAA	ACACATCGCC	CGCGCGGATG	TCGCGGCTGT	CGGTTACGAT
351	GCGCGACACG	GGTTTGCTTT	CAGACGGCAT	CGGAAGCTTG	AGGGCTTTGG
401	AGATGAAATT	TAGGTCAGT	GGTTTCATAT	TTACTTTCTG	TAATATTCGG
451	CGCGCGGACA	CATCGGTAGC	TGCTGATTTT	TTTATCGCCT	GGTTTGCTGT
501	GGTAAACAC	AGATTATTTT	CCCATTCTCA	TTCGGCATT	TTTCTGTACG
551	TATCATTTTT	TAGACGTATT	TTTAGTCGAT	TTGCCTTTTC	CCGATACCCA
601	CGCGCGGGGG	TCGTCGGGCA	GTCCTGCGAT	AAAGGCAAGG	TTATTGCTCT
651	CGCCCTGCAC	ATCGGGAACA	TTCCCCCAAA	AATCATAGCC	GTATCGGGC
701	AACTCGTCGG	TTTCGATACC	CGTCCAACTG	CCGAATCCGC	GTAA

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

a082.ppt

1	MWLLKLPAVA	KTALSPKRRR	NTAANISFTV	VLPPEPVI PN	TNGFTFSRHA
51	FANICNAVSV	SSTFVNAPSIA	TQSSRETTTA	AAPAAMTSSR	KSCASNRPPA
101	NAKNTSPARM	SRLSFVMRDT	GLLSDGHGSL	RAWQMKFSSS	GFIFTFVNRI
151	<u>AADTSVAADF</u>	<u>FIACFAVVKH</u>	RLFSDHGSFA	FLYVSFFERRI	FSRFAFSRIP
201	RRGVVGQSDV	KGKVIAFALH	IGNIPPKIIA	VIGQLVGFD T	RPTAESA*

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLPAVANTASSPKRRRNTAASISFTVVLPPPEVMPNTNGFTFSRHAFASVCNAASV					
a082	MWLLKLPAVAKTALSPKRRRNTAANISFTVVLPPPEVIPNTNGFTFSRHAFANICNAVSV					
	10	20	30	40	50	60
m082.pep	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRS PANAKNTSPARMSRLSVTMRDT					
a082	SSTFNAPSIIATQSSRETTTAAAPAANTSSTKSCASNRPANAKNTSPARMSRLSVTMRDT					
	70	80	90	100	110	120
m082.pep	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF					
a082	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF					
	130	140	150	160	170	180
m082.pep	FLYVSFFRRIFSRFAFSRI PRRGVVGQSVDKGKVIAFALHIGNIPPKIIAVIGQLVGFD					
a082	FLYVSFFRRIFSRFAFSRI PRRGVVGQSVDKGKVIAFALHIGNIPPKIIAVIGQLVGFD					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

g084.seq

1	ATGAAacaAT	CCGcccgaat	aAAAAATATG	GATCAGACAT	TAAAAAATAc
51	attgggcatt	tGCGCGcttt	tagcctTTTG	TTTTggcgcg	gccatCGCAT
101	CAGGTTATCA	CTTGGAATAT	GAATACGGCT	ACCGTTATTc	TGCCGTGGGC
151	GCTTTGGCTT	CGGTTGTATT	TTTATTATTA	TTGGCACGCG	GCTTCCCGCG
201	CGTTTCTTCA	GTTGTTTTC	TGATTTACGT	CGGCACAACC	GCCCTATATT
251	TGCCGGTCGG	GTGGCTGTAT	GGTGGCGCCT	CTTATCAGAT	AGTCGGTTCG
301	ATATTGAAAA	GCAATCCTGC	CGAGGCGCGT	GAATTTGTCTG	GCAATCTTCC
351	CGGGTCGCTT	TATTTTGTGC	AGGCATTATT	TTTCATTTT	GGCTTGACAG

g084 . pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084 . pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

	10	20	30	40	50	
m084.pep	MKQSARIKXMNQTLTYLGLICALLTF-----YHPEYEYGYRYSAVGALASVVFLLL					
	: :					
g084	MKQSARIKNMDQTLKNTLGICALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
	60	70	80	90	100	110
m084.pep	LARGFPRVSSVVLIIYVGTTALYLPGWLYGAPSYQIVGSILESNPAEAREFVGNLPSSL					
g084	LARGFPRVSSVVLIIYVGTTALYLPGWLYGAPSYQIVGSILESNPAEAREFVGNLPSSL					
	70	80	90	100	110	120
	120	130	140	150	160	170
m084.pep	YFVQALFFIFGLTVWKYCVS GGVFADVKNYKRRSKIWL TILLT LILSCAVMDKIASDKDL					
g084	YFVQALFFIFGLTVWKYCVS VGVFADVKNYKRRSKIWL TILLT LILSCAVMEKIAGDKDW					
	130	140	150	160	170	180

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	180	190	200	210	220
m084 . pep	REPDAGLLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX				
g084	REPDAGLLLLNIFDLYYDLAFRAGTICRQARPHFGSSKKSVMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGC GCGCTTT TAGCCTTTT TTTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTG TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCCG
301 ATATTGGAAT GCAATCCTGC CGAGGCGCGT GAATTTGTCT GCAATCTTCC
351 CGGGTCGCTT TATTTGTGTC AGGCATTATT TTTCATTTT GGCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTGTCT
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKNM DOTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWRYCVS GGVEADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMNQTLTYLTGICALLTFXXXXXXHYHPEYGYRYSAVGALASVVFLLL					
	: :					
a084	MKQSARIKNMDOTLKNTLGI CALLAFCFGA AIASGYHLEYEYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAREFVGNLPGSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	:					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
	190	200	210	220	230	
m084 . pep	REPDAGLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
a084	REPDAGLLNIFDLYYDLASXAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGT TGAAAGATAA

```

```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTCTAGA CCGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGCL NLTDCVTLEE
51  AVQTAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCCTG CGCGATGCAC TGGTAGGCAA
51  GGCAAAAGGC GTGTTCTTGA TTGGTGTCTGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCCGTTTCTAGA CCGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201 CAGCCCCGCC TCGCGGAGCT TTGATATGTT CAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGCL NMTDCATLGE
51  AVQTAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQAE					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGCLNLTDCVTLEEAVQTAYAQAE					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCCTG CGCGACGCGC TTGCCGGCAA
51  GGCAAAAGGC GTGTTCTCTGA TCGGTGTCTGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTCTAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51  AVQKAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIGA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQAE					

g086.seq

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

g086 . pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

m086.seq

1	ATGGTGGTGC	TGATGACGGC	GTTCAAGCTG	CTGATGATTT	ATTCGGCTTC
51	TGTGTATTGT	GCATCAAAAG	AAGCGGCGA	TCAGTTTTTC	TATTTGACCA
101	GACAGGCGGG	GTTCGTCGTT	GCCGCTTGA	TAGCAGCGG	TTTGTTATGG
151	TTTCTTTGCA	GGATGAGGAC	ATGGCGGCGG	CTTGTCGGT	GGATTTTTCG
201	CCTATCCGGC	CTGTTGCTGG	TAGTCGTATT	GATTGCCGGG	CGCGAAATCA
251	ATGGCGCGAC	CCGTTGGATA	CTTTGGGTC	CGTTGAATTT	CCAGCCGACC
301	GAGCTGTTCA	AGCTGGCGGT	CATCCTTTAT	TTGGCAAGCC	TGTTACGCGC
351	CCGTGAAGAA	GTGTTGCACA	GCATGGAAG	TTTGGGTTGC	CAGTCGATTT
401	GCGGGGGGAC	GGCCAATCTG	ATCATCTCCG	CCACCAATCC	GCAGrCACGT
451	CGTGAAACAT	TAGAAATGTA	CGGCCGTWTC	CGGCGATCA	TCCTGCCGAT
501	TATGCTGGTG	GCGTTCGGTT	TGGTGCTGAT	AATGGTACAG	CCGGATTTTCG


```

m086.pep      IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFFNIGVNIGALPXKGLTXP
                |||||||||||||||||||||||||||||||||||||||||:|||||
g086          IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFFNIGVNIGALPTKGLTLP
                310      320      330      340      350      360

                370      380      390
m086.pep      XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX
                |||||||||||||||||:|||||
g086          LMSYGGSSVFFMLISMMLLLRIDYENRQKMRGYRVEX
                370      380      390

```

a086.seq

This corresponds to the amino acid sequence <SEQ ID 276; ORF 086.a>:

a086.pcp

1	MVVLMTAFSL	LMIYSASVYL	ASKEGGDQFF	YLTRQAGFVV	<u>AGLIASGLLW</u>
51	FLCRMRTWRR	LVPWIFALSG	LLLVVVVLGQ	REINGATRWI	PLGPLNFQPT
101	ELFKLAVILY	LASLFTREEE	VLRSMESLWG	QSIWRGTANL	IMSAVTNPQAR
151	RETELMEYGRF	RAILFLPIMLV	AFGLVLIMVQ	PDFSGFVVIT	VIAVGMLFLA
201	<u>GLPWKYFFVL</u>	VGSVLGGMVL	MITAAPYRVQ	RVVAFDPWK	DPQGAGYQLT
251	HSLMAIGRGE	WFGMGLGASL	SKRGFLPEAH	TDFIFAIIEA	EFEGFGMCVL
301	IFCYGGLVVR	AFSINGQSRD	LGLTFNAYIA	SGIGIWIIGQ	SFFNIGVNIG
351	ALPTKGLTLP	LSMYGGSSVF	FMLISMMLLL	RIDYENRRKM	RGYRVE*

m086/a086 98.0% identity over a 396 aa overlap

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
a086	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASLFTREE					
a086	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASLFTREE					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESL	GWQSIWRGTANLIMS	SATNPQXRRETLEMYGR	XRAILPIMLVAFGLVL	IMVQ	
a086	VLRSMESL	GWQSIWRGTANLIMS	SATNPQARRETLEMYGR	FRAILPIMLVAFGLVL	IMVQ	
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVG	MLFLAGLPWKYFFVL	VGSVLGGMVLMITA	APYRVQRVVAFLD	PWK	
a086	PDFGSFVVITVIAVG	MLFLAGLPWKYFFVL	VGSVLGGMVLMITA	APYRVQRVVAFLD	PWK	
	250	260	270	280	290	300
m086.pep	DPQAGYQLTHSLMA	IGRGEWFGMGLGASL	SKRGFLPEAHTDFI	FAIIAEFEGFFG	MCVL	
a086	DPQAGYQLTHSLMA	IGRGEWFGMGLGASL	SKRGFLPEAHTDFI	FAIIAEFEGFFG	MCVL	
	310	320	330	340	350	360
m086.pep	IFCYGWL	VVRAFSIGKQSRDL	GLTFNAYIASGIGI	WIGXQSFNIGVNI	GALPKXGLTXP	
a086	IFCYGWL	VVRAFSIGKQSRDL	GLTFNAYIASGIGI	WIGIQSFNIGVNI	GALPTKGLTLP	
	370	380	390			
m086.pep	XMSXGGSSVFFML	ISMMLLXRIDYENRR	KMRGYRVEX			
a086	LMSYGGSSVFFML	ISMMLLLRIDYENRR	KMRGYRVEX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACACAT
51  TTTCCCAGCT CTGGCTGTGG CGGATTCATT GCGCGTGCGC GGTCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTTCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGCATAC GCTTGGAAC GCTGGCGATT AAAGGAATAC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TTCCGTTTAC TCTGTACAAA ACCGTCCGCG
251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGGTTTTCG TTACCTTTCC CGGCGGTCTG GCGGCGAAAC TCTTGGGCGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGCTTG TCCAACCGCC
401 AccTGTCGCG ctGGGCGAAA CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGTTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGCGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGTGCGG ACGTTTGTAA CAAAACCGTA
601 CCGCAGGCGT TGGCACTGCT GCCTGAAGAG GTGCGCCCGC AGATGTACCA
651 CCAGTCGGGG CGTAACAAGC TGGGCAATCT TCAGGCGGAT TATGACGCGT
701 TGGGCGTGAA AGCGGAATGC GTGGAATTTA TTACCGACAT GGTGTCCGCC
751 TACCGTGATG CCGATTGGT GATTTGCCGT GCCGGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGGC TGGGCGCGTT GTTAGTGCCG TATCCTCACG
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTCATGGT GCAGGCAGAA
901 GCGGGGCTGC TGTGCGGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 AATCCTCGGC AGCCTCAACC GCGAAAAATG CCTCAAATGG GCGGAAACG
1001 CCCGTACGTT GGCATTGCCG CACAGCGCGG ATGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRVR GHHVIWLGSK DSMEERIVPQ
51  YGIRLETIAI KGIRNGIKR KLMLPFTLYK TVREAQRIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLYAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQGREG RLKILVVGGS LGADVLNKTV

```

201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
 301 AGLLLPQTQL TAEKLAELG SLNREKCLKW AENARTLALP HSADDVAEAA
 351 IACAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq
 1 ATGGGCGGTA AAACCTTTAT GCTGawkkCG GCGGGAACGG GCGGACATAT
 51 TTCCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
 101 TGATTGGCT GGGCAGCAAG GATTCGATGG AAGAGCGTAT CGTGCCGCAA
 151 TACGGCATACT GCTTGGAAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
 201 CATCAAACGC AAATGATGC TGCCGGTTAC TTTGTATCAA ACCGTCGCGC
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
 301 GCGGCTTCG TTACCTTCCC CGGCGGTTTG GCGGCGAAGC TATTArGCGT
 351 GCGGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
 401 ACCTGTGCGC CTGGGCGAAG CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
 451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
 501 CTGCCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
 551 TTTTGGTGGT CGGCGGCAGT TTGGGCGCGG ACGTTTTGAA CAAAACCGTA
 601 CCGCATGCAT TGGCTTTGCT GCGCGACAAT GCGCGTCCGC ATATGTACCA
 651 CCAATCGGGA CGGGGCAAGC TGGGCATCTT GCAGGCGnnnn nnnnnnnnnn
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CGGTTGACGA
 801 TCACCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG GCGGGATTGC
 851 TGTGCGGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT
 951 GGCAGTCCG CACAGTGGC ACGACGTGGC GGAAGCCGCG ATTGCGTGTG
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep
 1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVHVLGSK DSMEERIVPQ
 51 YGIRLETLAI KGVGRNGIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF
 101 GGFVTFPGGL AAKLLXVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKT
 201 PHALALLPDN ARPHMYHQSG RGKLILQAX XXXXXXXXXXXX XXXXXXXXXXXX
 251 XAGLGALLVP YPHAVDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAELG
 301 GLNREKCLKW AENARTLALP HSADDVAEAA IACAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQYGIRLETLAI					
	: : : : :					
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVRGHHVHVLGSKDSMEERIVPQYGIRLETLAI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m087.pep	KGVGRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
	: : : : : :					
g087	KGIRGNGIKRKLMLPFTLYKTVEQAQRIIRKHRVECVIGFGGFVTFPGGLAAGLVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	: : : : :					
g087	IHEQNAVAGLSNRHLSRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180

279

	190	200	210	220	229
m087.pep	RLKILVVGGSLGADV	LNKTVPHALALLPDN	ARPHMYHQSGR	KGILQA-----	
g087	RLKILVVGGSLGADV	LNKTVQALALLPEE	VRPQMYHQSGRN	KLGNLQADYDAL	GVKAEC
	190	200	210	220	230
m087.pep	-----			AGLGALLVPYPH	AVDDHQTANARFMVQAE
g087	VEFITDMVSAYRDAD	LVICRAGALTIAEL	TAAGLGALLVPYPH	AVDDHQTANARFMVQAE	
	250	260	270	280	290
m087.pep	260	270	280	290	300
	AGLLLPQTQLTAEK	LAEILGGLNREK	CLKWAENARTLAL	PHSADDVAEAAIACAAX	
g087	AGLLLPQTQLTAEK	LAEILGSLNREK	CLKWAENARTLAL	PHSADDVAEAAIACAAX	
	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087.seq

1	ATGGGCGGTA	AAACCTTTAT	GCTGATGGCG	GGCGGAACGG	GCGGACATAT
51	TTTCCCCGCG	CTGGCGGTGG	CGGATTCATT	GCGCGCGCGC	GGCCATCATG
101	TAATTGGCT	GGGCAGCAAG	GATTCGATGG	AAGAGCGCAT	CGTGCCGCAA
151	TACGACATCC	TGCTCGAAAC	GCTGGCGATT	AAAGGCGTGC	GCGGCAACGG
201	CATCAAACGC	AAGCTGATGC	TGCCGTTTAC	TTTGTATCAA	ACTGTCCGCG
251	AAGCGCAGCA	GATTATCCGC	AAACACCGTG	TCGAGTGCGT	CATCGGCTTC
301	GGCGGCTTCG	TTACCTTTCC	CGGCGGTTTG	GCGGCGAAGT	TATTAGGCGT
351	GCCGATTGTG	ATTACAGAGC	AAAACGCCGT	GGCAGGTTTG	TCCAACCGCC
401	ACCTGTCGCG	CTGGGCGAAG	CGGGTGTTGT	ACGCTTTTCC	GAAAGCGTTC
451	AGCCACGAAG	GCGGCTTGGT	CGGCAACCCC	GTCCGCGCCG	ATATTAGCAA
501	CCTGCCCGTG	CCTGCCGAAC	GCTTCCAAGG	GCGTGAAGGC	CGTCTGAAAA
551	TTTTGGTGGT	CGGCGGCAGT	TTGGGCGCGG	ACGTTTTGAA	CAAAACCGTA
601	CCGAGGCAT	TGGCTTTGCT	GCCCCACAAT	GCGCGTCCGC	AGATGTACCA
651	CCAATCGGGA	CGGGGCAAGC	TGGGCAGCTT	GCAGGCGGAT	TACGACGCGC
701	TGGGCGTGCA	AGCGGAATGC	GTGGAATTTA	TTACCGATAT	GGTGTCCGCC
751	TACCGCGATG	CCGATTTGGT	GATTTGCCGT	GCCGCGCGCG	TGACGATTGC
801	CGAGTTGACG	GCGGCGGGAT	TGGGTGCGTT	GTTAGTGCCG	TATCCTCACG
851	CCGTTGATGA	CCATCAAACC	GCCAACGCGC	GTTTTATGGT	GCAGGCGGAG
901	GCGGGATTGC	TGTTGCCGCA	AACCCAGTTG	ACGGCGGAAA	AACTCGCCGA
951	GATTCTCGGC	GGCTTAAACC	GCGAAAAATG	CCTCAAATGG	GCAGAAAACG
1001	CCCGTACGTT	GGCACTGCCG	CACAGTGCGG	ACGACGTTGC	CGAAGCCGCG
1051	ATTGCGTG TG	CGGCGTAA			

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087.pep

1	MGGKTFMLMA	GGTGGHIFPA	LAVADSLRAR	GHHVIWLGSK	DSMEERIVPQ
51	YDILLET LAI	KGVRGNGIKR	KLMLPFTLYQ	TVREAQQIIR	KHRVECVIGF
101	GGFVTFPGGL	AAKLLGVPIV	IHEQNAVAGL	SNRHLSRWAK	RVLYAFPKAF
151	SHEGGLVGNP	VRADISNLPV	PAERFQREG	RLKILVVGGS	LGADV LNKT V
201	PQALALLPDN	ARPMYHQSG	RGKLSLQAD	YDALGVQAE	VEFITDMVSA
251	YRDADLVICR	AGALTIAELT	AAGLGALLVP	YPHAVDDHQT	ANARFMVQAE
301	AGLLLPQTQL	TAEKLAEILG	GLNREKCLKW	AENARTLALP	HSADDVAEAA
351	IACAA*				

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIWLGSKDSMEERIVPQYGIRLET LAI					
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVIWLGSKDSMEERIVPQYDILLET LAI					
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVGRNGIKRKLMPLVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVGRNGIKRKLMPLFTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAEC					
	190	200	210	220	230	240
	250	260	270	280		
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

g088.seq

1	ATGTTTTTAT	GGCTCGCACA	TTTCAGCAAC	TGGTTAACCG	GTCTGAATAT
51	TTTTCAATAC	ACCACATTCC	GCGCCGTTAT	GGCGGCGTTG	ACCGCCTTGG
101	CGTTTTCCCT	GATGTTCCGC	CCGTGGACGA	TACGCAGGCT	GACCGCGCTC
151	AAATGCGGGC	AGGCAGTGCG	TACCGACGGC	CCGCAAACCC	ACCTCGTCAA
201	AAACGGCACG	CCGACGATGG	GCGGTTTCGCT	GATTCTGACC	GCCATTACCG
251	TGTCCACCCT	GTTGTGGGGC	AACTGGGCGA	ACCCGTATAT	CTGGATTCTC
301	TTGGGCGTAC	TGCTTGCCAC	CGGTGCGCTC	GGTTTTTACG	ACGACTGGCG
351	CAAAGTCGTT	TATAAAGACC	CCAACGGCGT	GTCCGCCAAA	TTCAAAATGG
401	TGTGGCAGTC	AAGCGTTGCC	GTTatcgCG	GTttggcaTT	GTTTTACctt
451	gCcgCAATT	CCGCCAACAA	TATTTTGATT	GTCCCGtttT	TCAACAAAT
501	CGCCCTGCCG	CTGGGCGTGG	TCGGCTTttt	gGtgttgTCT	TACCTGACCA
551	TCGTCCGGCAC	ATCCAACGCC	GTCAACCTCA	CcgaCGGCTT	GGACGGCCCT
601	GCCGCcttcc	cgttcgctcc	cgttgcgcgC	GGGCTCGCCA	tttccgctTA
651	CGTCAGCGGA	CACTACCAAT	TTTCCAATA	CCTCCAGCTT	CCCTATGTCG
701	CCGGCGCGAA	CGAAGTCGCT	ATATTCTGCA	CCGCCATGTG	CGGCGCGTGC
751	CTCGGATTTT	TGTGGTTCAA	CGCCTATCCC	GCGCAAGTCT	TTATGGGCGA
801	TGTCGGCGCG	CTGGCATTGG	GTGCCGCGCT	CGGTaccGtt	gCCGTcaTcg
851	tCCGCCAAGA	ATTTGTcctc	gtcattaTGG	GCGGTCTGTT	cgtcgtagaa
901	gccgtgTCCG	TTATGCTTCa	tgctcgCTGG	TACAAGAAAA	Ccaaaaaacg
951	CATCTTcCTg	acgGcaccga	ttcatcacca	ttaCCAactt	cgatgCTGGa
1001	aagaaacgca	agtcgtcgct	CGTtCTGGA	TTAtTaccat	cgtcgtggtt
1051	tTgatagggt	tGagtacccT	caAAattcgc	ggaaactatg	ccgTCCGAAC
1101	ACCTTTCAGA	CGGCATTGGA	ACGCGCAATA	A	

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

g088.pep

1	MFLWLAHFSN	WLTGLNIFQY	TFRAVMAAL	TALAFSLMFG	PWTIRRLTAL
51	KCGQAVRTDG	PQTHLVKNGT	PTMGGSILIT	AITVSTLLWG	NWANPYIWL
101	LGVLLATGAL	GFYDDWRKVV	YKDPNGVSAK	FKMVWQSSVA	VIAGLALFYL
151	AANSANNILI	VPPFKQIALP	LGVVGFLVLS	YLTIVGTSNA	VNLTDGLDGL

281

201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

m088.seq

1 ATGTTTTTAT GGCTCGCACA TTTCAGCAnC TGGTTAACCG GTCTGAATnn
 51 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 101 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 151 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 201 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 251 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 301 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 351 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 401 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 451 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 501 nnnnnnnnnnnn nnnGGCGTGG TCGGCTTTTT GGTGTTGTCT TACCTGACCA
 551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT
 601 GCGACCTTCC CCGTCGTCTT CGTTGCCGCC GGCCTCGCCA TCTTCGCCTA
 651 TGCCAGCGGC CACTCACAAAT TTGCCCAATA CCTGCAATTA CTTTACGTTG
 701 CCGGCGCAAA CGAAGTGGTG ATTTTCTGTA CCGCCATGTG CGGCGCGTGC
 751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
 801 TGTCCGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGTC GCCGTATCG
 851 TCCGCCAAGA GTTTGTCTCT GTCATTATGG GCGGATTATT TGTCGTAGAA
 901 GCCGTATCCG TTATGCTTCA GGTGCGCTGG TATAAGAAAA CCAAAAAACG
 951 CATCTTCCTG ATGGCGCCCA TCCATCACCA CTACGAACAA AAAGGCTGGA
 1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGGG TTATTACCAT CGTCTTGGTG
 1051 TTGATCGGTT TGAGTACCCT CAAAATCCGC TGAACCTATG CCGTCTGAAC
 1101 ATCTTTCAGA CGGCATTGGA ACGCGCAATA A

1 MFLWLAHFSN WLTGLNIFOY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
 51 KCGQAVRTDG PQTHLVKNGT PTMGGSLILT AITVSTLLWG NWANPYIWIL
 101 LGVLLATGAL GFYDDWRKV YKDPNGVSAS FKMVWQSSVA VIAGLALFYL
 151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTGDLGL
 201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

m088.pep

1 MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 101 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 151 XXXXXXXXXXX XXXXXXXXXXX XGVVGFLVLS YLTIVGTSNA VNLTGDLGL
 201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
 301 AVSVMLQVGW YKKTKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV
 351 LIGLSTLKIR XTYAVXTSFR RHLNAQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/g088

m088.pep
 10 20 30
 GVVVGFLVLSYLTIVGTSNAVNLTGDLGLA
 |||||
 g088 IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGLA
 150 160 170 180 190 200

	40	50	60	70	80	90
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVI FCTAMCGACLGFLWFNAYPA					
	: : : :					
g088	AFFPVLVAAGLAIFAYVSGHYQFSQYLQLPYVAGANEVAIFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	100	110	120	130	140	150
m088.pep	QVFMGDVGALALGAALGTAVIVRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
	:					
g088	QVFMGDVGALALGAALGTAVIVRQEFVLVIMGGFLVVEAVSVMLHVGWYKTKKRIFLT					
	270	280	290	300	310	320
	160	170	180	190	200	
m088.pep	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
	: : :					
g088	APIHHHYQLRCWKETQVVVRFWIITIVVVLIGLSTLKIRGNYAVRTPFRRLNAQX					
	330	340	350	360	370	

```

a088.seq
1 ATGTTTTTAT GGCTCGCACA TTTCAGCAAC TGGTTAACCG GTCTGAATAT
51 TTTTCAATAC ACCACATTCC GCGCCGTCAT GCGCGCGTTG ACCGCGCTGG
101 CGTTTTCCCT GATGTTCCGG CCGTGGACGA TACGCAAGGT GACCGCGCTC
151 AAATGCGGGC AGGCAGTGCG TACCGACGGT CCGCAAACCC ACCTCGTCAA
201 AAACGGCACG CCGACGATGG GCGGTTGCT GATTCTGACC GCCATTACCG
251 TGTCCACCTT GTTGTGGGGC AACTGGGCAC ACCCGTATAT CTGGATTCTC
301 TTGGGCGTAT TGCTCGCCAC GGGCGCACTT GGTTTTATAG ACGACTGGCG
351 CAAAGTCGTC TATAAAGACC CCGACGGCGT GTCCGCCAAA TTCAAAATGG
401 TGTGGCAGTC AAGCGTTGCC ATTATCGCCG GTTTGGCATT GTTTTACCTT
451 GCCGCCAATT CCGCCAACAA TATTTTGATT GTCCCGTTCT TCAAACAAAT
501 CGCCCTGCCG CTGGGCGTGG TCGGCTTTTT GGTGTTGTCT TACCTGACCA
551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT
601 GCGACCTTCC CCGTCGTCTT CTTGCGCGCC GCGCTCGCCA TCTTCGCCTA
651 TGCCAGCGGC CACTCACAAT TTGCCCAATA CCTGCAATTA CCTTACGTTG
701 CCGGCGCAA CGAAGTGGTG ATTTTCTGTA CCGCCATGTG CGGCGCGTGC
751 CTCGGTTTCT TGTGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTGCGTGCA TTGGCATTTG GTCCCGCGCT CCGTACCGTC GCGCTCATCG
851 TCCGCCAAGA GTTGTCTCTT GTCATTATGG GCGGATTATT TCTCGTAGAA
901 GCCGTATCCG TTATGCTTCA GGTGGGCTGG TATAAGAAAA CCAAAAAACG
951 CATCTTCTTG ATGGCGCCCA TCCATCACCA CTACGAACAA AAAGGCTGGA
1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGGA TTATTACCAT CGTCTTGGTG
1051 TTGATCGGTT TGAGTACCTT CAAATCCCGT TGAACCTATG CCGTCTGAAC
1101 ACCTTTTCAGA CGGCATTTGA ACGCGCAATA A

```

a088.pep

1	MFLWLAHFSN	WLTGLNIFOY	TTFRVMAAL	TALAFSLMFG	PWTIRRLTAL
51	KCGQAVRTDG	PQTHLVKNGT	PTMGSSLILT	AITVSTLLWG	NWANPYIWL
101	<u>LGVLATGAL</u>	<u>GFYDDLWRKV</u>	<u>YKDPNGVSAK</u>	<u>FKMVQSSVA</u>	<u>IAGLAIWYL</u>
151	AANSANNILI	YPFFKQIALP	LGVVGFVLVS	YLTIVGTSNA	VNLTDLGLDGL
201	<u>ATFPVVLVAA</u>	<u>GLAIFAYASG</u>	<u>HSQFAQYLQL</u>	<u>PYVAGANEV</u>	<u>IFCTAMCGAC</u>
251	<u>LGFLWFNAYP</u>	<u>AQVFMGDVGA</u>	<u>LALGAALGTV</u>	<u>AVIVRQEFVL</u>	<u>VIMGGLFVVE</u>
301	<u>AVSVMLQVGW</u>	<u>YKTKTKKRIFL</u>	<u>MAPIHHHYEQ</u>	<u>KGWKETQVVV</u>	<u>REWIITIVLV</u>
351	LIGLSTLKIR	*TYAV*TPFR	RHLNAQ*		

m088.pep XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFLVLSYLTIVGTSNAVNLT DGLDGLA
|||||
a088 IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLT DGLDGLA

283

	150	160	170	180	190	200
	210	220	230	240	250	260
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088.pep	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088.pep	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

```

g089.seq
1  ATGCCGCCCA AAATCACGAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACACGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGGCA GCCATAACGT TGGCGGCGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTGCGT AGAAATCAAA TCTTCATTGC CTTGTTTAA ACAGCCCCTC
301 CCGCGTTCCA ACCAAAAATC GGCTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAAATCT CGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

```

g089.pep
1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKTCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

```

m089.seq
1  ATGCCGCCCA AAATCACKAw GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwA
251 TGTCTTGCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

```

m089.pep
1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSI NTTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng) from *N. gonorrhoeae*:

m089/g089

284

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPTFVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSNASRD					
	: : : : :					
g089	MPPKITXSGFCKPAIAAAVAPTFVPLLSSMNTTPFFSPIFSTRCGRPWKVLTCSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : : :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSLPCFKQPVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

```

1  ATGCCGCCTA AAATCACGAA GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GCGGGTCGCA CCGACGTTCG TGCCTTTGCT GTCGTCGATG AACACCACGC
101 CATTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGAAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGGC AAACCGACGG CTTCGCACAA
201 GGCAACGGCA GCCATCACGT TAGTGGCGTT GTGCAAGCCT TGCAGCGGAA
251 TATCTTGCGT GGCAATCAAA TCTTCATTGC CTTGTTTCAG GCGACCTGTC
301 TCACGTTCCA ACCAAAAATC GGCTTCGTAT TCCAACGAAA ACCATTTTCA
351 CTCGCGCCCG GCGCGCTTCA TCGCACGACA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC ACCGTCGCCA CGGAAAATCT TGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

```

1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTPFFSPIF STRCGRP*KV
51  LTCSSNASRG KPTASHKATA AITLVALCKP CSGISCVAIK SSLPCFRRPV
101 SRSNQKSASY SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPTFVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSNASRD					
	: : : : :					
a089	MPPKITXSGFCKPAIAAAVAPTFVPLLSSMNTTPFFSPIFSTRCGRPXKVLTCSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : : :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSLPCFRRPVSRNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

```

1  ATGCGCGTAG TCGAGCAAAT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA

```

g090 . pep

m090.seq

m090 . pep

m090/g090

a090.seq

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

286

a090.pep

```

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
51 LQFRLQNRRA DIARDNGIQP TLDAEIADQA RYRGFAVAAG NRNHLVAAAV
101 HNVRRQQFDVA QHAXRRFA*

```

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAF	GVFQLEAGKLQ	HPHVRLFAFA	LPFRLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAF	GVFQLETGKLQ	HPHVRLFAFA	LQFRLQNRRA
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQP	ALDTEIADQ	ARYRGFAVA	AGNRNLYV	PAVHNVRR	QQFDVAQHAXRRFAX
a090	DIARDNGIQP	TLDAEIADQ	ARYRGFAVA	AGNRNHLV	AAAVHNVRR	QQFDVAQHAXRRFAX
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:**m090-1.seq**

```

1 ATGACGGCGT TTGCATTTCA GACGGCATCA CAAAGCCTTA AACGCTTCGA
51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC
151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
201 AGCCGTCCAA ATCGCGGCGG ATTTGCGGCG CATCGACACC AATCAAGAAC
251 ACGCCTTTTG CCTTGCCTAC CAGTGCATCG CGCAGGGGCG TGAAGTCCTG
301 CCCTTTACCC ATGCCGCCCA AAATCACGAA GAGCGGATT TGCAAACCGG
351 CAATCGCGGC GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA
401 AACACCACGC CGTTTTTCTC GCCGATTTTT TCCACGCGGT GCGGCAGGCC
451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGGCGTT GTGCAGACCT
551 TGCAACGGAA TGTCTTGCGT GACAATCAAA TCTTCATTGC CTGTGTTTCA
601 GCGGCCTGTC TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
651 ACCATTTTAC CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
701 TCCGCATTCA AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGCTTTGGT
751 ATCGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGA
801 TGTTCAGCAC CGTCGCCGCA GTCGGACGCA GGCTTTCGTT GTTTCCAGT
851 TGGAAGCTGG AAAGCTCCAA CACCCACACG TCCGCCTTTT TGCCTTCGCG
901 CTGCCATTCC GCCTCCAAA CCGCGGTGCC GATATTGCC GCGATAACGG
951 TATCCAGCCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG
1001 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTGTGCT CCCGCGGTT
1051 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT CCGCCGTTT
1101 GCTTGAACGC CTCAATATCC GGCTGCCGCT CGCTGATGCC GGGACTGAGA
1151 GCAGAAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGA
1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCCGGCT
1251 TCAGCTCCGC ATCATACGCA GCAACCTCCG CGCCGTTTTT GCGCAGGTAG
1301 GCAATCATGG AAATACCCGT ACCGCCGAGT CCGCGCAGCA GGATTTTTTT
1351 GTTTTGAAAA GTCATTTTGG TTTGTCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

m090-1.pep

```

1 MTAFAFQTAS QSLKRFDKHF RTVRVAFEDI KARAGGAEQH NIACFGLGIC
51 RLNGFSQSGA VGHIAAAVQ IAADLRRIDT NQEHAFCLAY QCIAQGREVL
101 PFTHAAQNH ERLQGTGNRG GSRADIRAF VVDKHHAVEL ADFFHAVRQA
151 LEGFDVFQEC FARQTDGLTQ SHGSHDVSGV VQTLQRNVLR DNQIFIALFO
201 AACLAFOPEI SFVFORKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFG
251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNLYVPAV
351 HNVRRQQFDVA QHASAVLLER LNIRLPLADA GTESQNIETV VQRIFQTARV
401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVE AQVGNHGNTR TAESGDEDF
451 VLKSHFGLS*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 303>:

g091.seq

```

1  ATGGAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  AAGTCATTTT GGTTTTGTCC TAAAACAAAT CATATTGGGC AGGAGACGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCCG ATTAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTCGCAGCT GTTTGGTCT CCGTTTGTAC
201 AAGCCTTGCC AAGCCATTGT TGAGCGAGCG CAAGGTCTTG GCGCACGCCG
251 CGTCCATCGT AATACATCAA GCCCAAATTG TATTGGGCTT GGGCATCCCC
301 TTGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

g091.pep

```

1  MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
51  RLQALVIVAA VLVSVLTSLA KPILLSERKVL AHAASIVIHQ AQIVLGLGIP
101  LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 305>:

m091.seq

```

1  ATGGAATAC CCGTACCGCC GAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  AAAGTCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGAGATGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTCGCAGCC GTCTTGGTCT CCGTTTGTAC
201 AAGCCTTGCC AAACCATCTT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATACATCAC GCCCAAATTG TTTTGGGCTT GGGCTACCCC
301 CTGCGC...

```

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

m091.pep

```

1  MEIPVPPSPA TRIFLFEKSF WFVLKQIILS RRCPPPLPKPL SDGIASCSIT
51  RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYP
101  LR.

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRIFLFEKSFWFVLKQIILSRRCPPPLPKPLSDGIASCSITRLQALVIVAA					
	: :					
g091	MEIPVPPSPATRIFLFESHFGFVLKQIILGRRPPPLPKPLSDGIASRLITRLQALVIVAA					
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQAQIVLGLGYPLR					
	: : : :					
g091	VLVSVLTSLAKPILLSERKVLHAASIVIHQAQIVLGLGIPLEX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

a091.seq

```

1  ATGGAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  GAAATCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGGGATGTC
101 TGATCCTGCT CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCTTTCAGG CGTTGGTCAT TGTCGCAGCT GTCTTGGTAT CCGTTTGTAC
201 AAGCCTTGCC AAGCCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATACATCAC GCCCAAATTG TTTTGGGC

```

This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLWKSF WFVLKQIILS RGCLILLKPL SDGIASCSIT
51 RFQALVIVAA VLVSVLTSIA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRI	FLFEKSFWFVLKQIILS	RRCPLPKPLSDGIASCSIT	RLQALVIVAA		
a091	MEIPVPPSPATRI	FLFEKSFWFVLKQIILS	RGCLILLKPLSDGIASCSIT	RFQALVIVAA		
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSIAKPFLCKGAVL	AHAASFGIHHAQIVLGLGYPLR				
a091	VLVSVLTSIAKPFLCKGAVL	AHAASFGIHHAQIVLG				
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGCGC
51  AAACGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCGGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGCATTCAA GTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCTCTACC GCCGTCAAGA AAGAAaatcC
351 CGAAGTtgtc gcTGCgTTGG AGCGGCAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGGcatcgc cattgcggT
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACTC AACGCCGCGC
551 GCACCAACGC CCGCTTGGGC AAAGCGGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTATCGAT TTCATCCACC GTATGCCCTT CTACGCCAAA
751 GCCTTTTTGT GTGTTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAAA AaggCTTGCT CGGCTTTGAA
1051 GGCGTCGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGAAAAA acgtTTGGTG
1201 CtgcCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatgC GCTGGTACTG ACCGAAGTTT
1301 AtgcgcgcgG CGAAGAGCCG GTTGCCGCCG CCGactcCG CGCCTTGCGC
1351 CGTGCTATCC GCGTATTGGG CAACTTGAG CCGATTACT GCGAAAtgt
1401 cgccgACCTG CCGCAATGC TGATGAATGT TTTACAGGAT Ggcgatgtg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgtg
1501 gaattgtcga AACAGAtttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
51  IGGVGMMSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHATAEHV
101 NGADV VVAST AVKKENPEVV AALERQIPVI PRALMLAELM RFRDGIATAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```

```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKTIVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCTTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTTGTCTGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGCAG
551 GACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATGCGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GCGCTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCTT TGCCGCCGCA CGCGCGCGT ATCTGGAAAA ACGTTTGGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CCGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GCGACATCG
1451 TGTTGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERINIMMK NRVNTNIHFVG
51 IGGVGMGSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKNPEVV AALEQQIPVI PRALMLAELM RFRDGLAIAAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKTIVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

```

m092/g092
10 20 30 40 50 60
m092.pep MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERINIMMKNRVTNIHFVGIGGVGMGSGIA

```

a092.seq

1	ATGTTTTTTT	TTTCAATCCG	CTATATATTT	GTCAGAAAAC	TATGGCGCGC
51	AAACGGTCAG	CCCTTTTAAA	TAACGCCTTT	ACGCATCGAA	AATCCACCGG
101	AACGCAACAT	TATGATGAAA	AAATCGAGTGA	CCAACATCCA	TTTTGTCCGT
151	ATCGGCGGCG	TCGGCATGAG	CGGTATCGCC	GAAGTCTTGC	ACAAATTGGG
201	TTTTAAAGTT	TCCGGTTCGG	ATCAGGCGCG	AAATGCCGCT	ACCGAGCATT
251	TGGCGACGCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGC	AGAACACGTT


```

301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT T GCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCGAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCAGACCT TTCCGCCGCA CGCGGCGCGT ATCCGGAAAA ACGTTTGGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCGCG ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTTGAACGT TTTGCAGGAC GGCGACATCG
1451 TGTTGAATAT GGGTGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

a092.pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIATAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKL PNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDETK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ELSKQI*

```

m092/a092 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVMSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVMSGIA					
	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
	130	140	150	160	170	180
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTSLTASILGAAGLDPTFVIGGKL					
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
	250	260	270	280	290	300
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
a092	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
	310	320	330	340	350	360
m092.pep	QMKGHEQGSFEVVLNMPGRHNVNLAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNLAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
	370	380	390	400	410	420
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLA FQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLA FQPHRYTRTRDLFEDFTK					
	430	440	450	460	470	480
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	490	500				
m092.pep	GDIVLNMGAGSINRVPAALLALSQIX					
a092	GDIVLNMGAGSINRVPAALLELSQIX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

g093.seq

```

1  aTGCAGAAAtt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgcTGGACA GCgGTACCGC CATTTTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGCGGAA GACGGGGCTG TTCAGGGTGC ATTGGAAGTGTG TGGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTGGCA GGCATTGGGA TTACCCGTTC CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTTCGATGC CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggtta
451 aAAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAaaCA
501 CCTTcagggg cgaAAtcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaaCCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGCG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

m093.seq

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKEKGRLLS VYEELKHLQG RNHCRTFYRR RRIFLPRPER QRAARHTHHP
201 RNRVLRRLRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSRTGNRCGRRLR
251 ARFPQRYRR QTLVGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCrAA GACGGGGCGG TTCAGGTGTC ATTGGAAGT TTGGGCATTTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGCGCA GGCATTGGGA TTGCCCCTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGCTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATAC ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGCG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

```

m093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRIFLPRPER QRAARHTHS
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RAGNRCGRLR
251 ARRFQRYRR QTLVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
	:					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKERGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLH					
	:					
g093	FNILHGTYGEDGAVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV KVKGKGR LKSVYEELKHLQX RNHCRTFYRR					
g093	DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV KVEKGR LKSVYEELKHLQGR RNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRIFLPRPER QRAARHTHS RNRVLR LRSQVQPRRHLSM SFGRFDRSRR KPDARTGGS R					
g093	RRIFLPRPER QRAARHTHS RNRVLR LRSQVQPRRHLSM SFGRFDRSRR KPDARTGGS R					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGRLR ARRFQRYRR QTLVGNQHP ARYDEPX					
	: :					
g093	RTGNRCGRLR ARRFQRYRR QTLVGNQHP ARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

a093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAACG TTGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATG CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CCGCGAATAT
551 TCCTGCCCTG TGTTGAACGG CAAAGGCCTG CCCGGCATA ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCTCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AEGSSVGVV
151 KVKGKGR LKS VYEELKHFQX RNHCRTVYRR RRIFLPCVER QPARHTHHP
201 RDRV L* LRSQ VQQRHHL SM SFG RSDRSRR KPDARTGGS R RAGNRCGR LR
251 ARRF PQRYRR QTL SVGNQH P ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
a093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
	10	20	30	40	50	60
m093.pep	FNILHGTYGDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
a093	FNILHGTYGEDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
	70	80	90	100	110	120
m093.pep	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGR LKS VYEELKHLQXRNHCRTFYRR					
a093	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGR LKS VYEELKHFQXRNHCRTVYRR					
	130	140	150	160	170	180
m093.pep	RRI FLRPERQRAARH THSRN RVLRLRSQVQPRRHLSMSFGRFDRSR RKP DARTGGS R					
a093	RRI FLPCVERQ RPARH THPRD RVLX LRSQVQQRHLSMSFGRSDRSRR KPDARTGGS R					
	190	200	210	220	230	240
m093.pep	RAGNRCGR LRARRFPQRYRRQ T LSVGNQH PARYDEPX					
a093	RAGNRCGR LRARRFPQRYRRQ T LSVGNQH PARYDRPX					
	250	260	270			

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 323>:

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

```

              10      20      30      40      50      60
m094.pep     MYSPLPKRALVPAALSLPPIITKVGSSPAAPRMEAVRLVVVVLPVCPAMAMPSRKRINSAN
              |||||||||||||||||||||||||||||||||||||||||||||:|:|
g094          MYSPLPKRALVPAALSLPPIITKVGSSPAAPRMEAVRLVVVVLPVCPAMAMPSRKRISSAS
              10      20      30      40      50      60

              70      80      90      100
m094.pep     IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
              |:|||||||||||||||:|||||
g094          IKARGITGICRSNAATTSGFSFLTAVEATTTTSAPLTCSAVWPGX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

This corresponds to the amino acid sequence <SEQ ID 326; ORF 094.a>:

1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51 PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCNAV
101 WPG*

	10	20	30	40	50	60
m094.pep	MYSPLPKRALVPAALSLP	PITKVGSSPAAPRMEAVRLVVVVLP	PCVPAMAMPSRKRINSAN			
a094	MYSPLPKRALVPAALSLP	PITKVGSSPAAPRMEAVRLVVVVLP	PCVPAMAMPSRKRINSAN			
	10	20	30	40	50	60
	70	80	90	100		
m094.pep	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTC	SAVWPGX				
a094	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTC	SAVWPGX				
	70	80	90	100		

g095.seq

1	ATGTCCTTTC	ATTTGAACAT	GGACGGTGAA	TTTCATTTGC	GCGCCGACGT
51	TTTCGATGTC	GGTGGCGTAG	ATGTCGGCGG	TATCGTCCAA	ACCGTAAGTA
101	GCATAAGGTT	TGCTCACTTT	GGGCAAATC	GCGCGGACGT	GTTCGCTGTC
151	AACACACAAA	AAGGCTTTGC	CGTAGAAGGG	CATACGGTGG	ATGAAATCGA
201	TAAACGCCTG	ATGCAGTTTT	TCGACGCTGT	GCCCGTAGGT	ATCCATATGG
251	TCTTCGTCGA	TATTGGTAAC	GACGGACATA	ATCGGGGTCA	GTGTAGGAAA
301	GAGGCATCGG	ATCGTCGGCT	TCGGCAACGA	TGTATTCGCC	TTTGCCCAAG
351	CGGGCGTTGG	TGCTCGCGGC	GTTGA		

g095 . pep

```

1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRAVDFAV
51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRGQCRK
101 EASDRRLRQR CIRLCPSGRW CLRR*

```

m095.seq

1	ATGTCCTTTC	ATTGAACAT	GGACGGTGAA	TTTCATTTGC	GCGCCGACGT
51	TTTCGATGTC	GGTGGCGTAG	ATGTCGGCGG	TATCGTCCAA	ACCGTAAGTA
101	GCATAAGGTT	TGCTCACTTT	GGGCAAAATC	GCGCGGACGT	GTTCGCTGTC
151	AATACACAAA	AAGGCTTTGC	CGTAGAAGGG	CATACGGTGG	ATGAAATCGA
201	TAAACGCCTG	ATGCAGTTTT	TCGACGCTGT	GCCCGTAGGT	ATCCATATGG
251	TCTTCGTCGA	TATTGGTAAC	GACGGACATA	ATCGGTGTCA	GTGCAGAAAG
301	GATGCATCCG	ACCGTCGGCT	TCGGCAACGA	TGTATTCGCC	TTTGCCCAAG
351	CGGGCGTTAG	TGCCTGCGGC	GTTGA		

m095 . pep

1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADEVFAV
51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRCQCRK
101 DASDRLRLROR CIRLCPSGRX CLRR*

Homology with a predicted ORF from *N. gonorrhoeae*

m095/q095

m095 . pep MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGF AVEG

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||:|||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
  1  ATGTCCTTTC  ATTTGAACAT  GGACGGTGAA  TTTCATTTGC  GCGCCGACGT
 51  TTTTCGATGTC  GGTGGCGTAG  ATGTCGGCGG  TATCGTCCAA  ACCGTAAGTA
101  GCATAAGGTT  TGCTCACTTT  GGGCAAAATC  GCGCGGACGT  GTTCGCTGTC
151  AATACACAAA  AAGGCTTTGC  CGTAGAAGGG  CATACGGTGG  ATGAAATCGA
201  TAAACGCCTG  ATGCAGCTTC  TCAACACTGT  GCCCGTAGGT  ATCCATATGG
251  TCTTCGTCTGA  TATTGGTAAC  GACGGACATA  ATCGGTGTCA  GTGCAGAAAG
301  GATGCATCCG  ACCGTCGGCT  TCGGCAACGA  TGTATTGCGC  TTTGCCCAAG
351  CGGGCGTTGG  TGCCTGCGGC  GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
  1  MSFHLNMDGE  FHLRADVFDV  GGVDVGGIVQ  TVSSIRFAHF  GQNRADVFAV
 51  NTQKGFAVEG  HTVDEIDKRL  MQLLNTVPVG  IHMFVDIGN  DGHNRCQCRK
101  DASDRRLRQR  CIRLCPSGRW  CLRR*

m095/a095  96.0% identity in 124 aa overlap

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||:|||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||:|||||
a095      HTVDEIDKRLMQLLNTVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
  1  ATGCCCGGTC  ATACCGGGCA  GGGTGTGAT  TTCCAACAGA  TAGAGTTTGC
 51  CGTCGGTATC  TTTGAGGAAA  TCGACGCGCA  CGCAGCCTTC  CGCACCATT
101  GCCTGTGCGC  CGCGAACCGC  CAGTTCGCGC  ATCAGGCTTT  CTTCGGCTTC
151  GGTCAAATCT  TCCGAAGGAC  ATTGAtaaat  ggtgTCGTCT  CGGttgtaCt

```

```

201  tggcttcgta  gTCGTAAAC  TCGGTTGCGG  GGATGATGTG  TATGCCGGGC
251  AGCCCTTTGC  CGTTCAGGAC  GGGGCAGGAA  TATTCGCCGC  CGCCGATAAA
301  AcgtTcggca  atgaTTtcgc  ccctgAAGGT  GttTCAattc  ttcgtaAACG
351  CTTTTCAGAc  ggccttTTTC  TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 334; ORF 096.ng>:

g096.pep

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHAARFRTDCLCAANRQFAHQAFFGFG
51  GQIFRRTLIN  GVVSVVLGFV  VVKLGCGDDV  YAGQPFQAVQD  GAGIFAAADK
101 TFGNDFAXEG  VSILRKRFSD  GLFL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 335>:

m096.seq

```

1  ATGGCTCGTC  ATACCGGGCA  GGGTGTGAT  TTCCAACAGA  TAGAGTTTGC
51  CGTCGGTATC  TTTGAGGAAA  TCGACGCGCA  CGCAGCCTTC  CGCACCATT
101 GCCTGCGCGC  CGCGAACC GC  CAGTTCGCGC  ATCAGGCTTT  CTTCGGCTTC
151 GGTCAAATCT  TCCGAAGGAC  ATTGATAAAT  GGTGTCGTCG  CGGTTGTACT
201 TGGCTTCGTA  GTCGTAAAC  TCGGTTGCGG  GAATGATGTG  TATGCCGGGC
251 AGCCCTTTGC  CGTTCAGGAC  GGGGCAGGAA  TATTCGCCGC  CGCCGATAAA
301 ACGTTCGGCA  ATGATTTTCG  CC.TGAAGGT  GTTTCATTC  TTCGTAAACG
351 CTTTTCAGAC  GGCCTTTTCC  TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 336; ORF 096>:

m096.pep

```

1  MARHTGQGVDFQQIEFAVGI FEEIDAHAARFRTDCLRAANRQFAHQAFFGFG
51  GQIFRRTLIN  GVVAVVLGFV  VVKLGCGNDV  YAGQPFQAVQD  GAGIFAAADK
101 TFGNDFAXEG  VSILRKRFSD  GLFL*

```

m096/g096 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGI FEEIDAHAARFRTDCLRAANRQFAHQAFFGFGQIFRRTLIN					
	:					
g096	MAGHTGQGVDFQQIEFAVGI FEEIDAHAARFRTDCLCAANRQFAHQAFFGFGQIFRRTLIN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPFQAVQDGAGIFAAADKTFGNDFAXEGVSILRKRFSD					
	:					
g096	GVVSVVLGFVVVKLGCGDDVYAGQPFQAVQDGAGIFAAADKTFGNDFAXEGVSILRKRFSD					
	70	80	90	100	110	120
m096.pep	GLFLX					
g096	GLFLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 337>:

a096.seq

```

1  ATGGCCGGTC  ATACCGGGCA  GGGTGTGAT  TTCCAACAGA  TAGAGTTTGC
51  CGTCGGTATC  TTTGAGGAAA  TCGACGCGCA  CGCAGCCTTC  CGCACCATT
101 GCCTGCGCGC  CGCGAACC GC  CAGTTCGCGC  ATCAGGCTTT  CTTCGGCTTC
151 GGTCAGATCT  TCCGAAGGAC  ATTGATAAAT  GGTGTCGTTG  CGGTTGTACT
201 TGGCTTCGTA  GTCATAAAC  TCGGTCGCGG  GGATGATGTG  TATGCCGGGC
251 AGCCCTTTGC  CGTTCACAC  AGGGCAGGAA  TATTCGCCGC  CGCCGATAAA
301 CCGTTCGGCA  ATGATTTTCG  CCT.GAAAGT  GTTTCATTC  TTCGTAAACG
351 CTTTTCAGAC  GGCCTTTTCC  TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 338; ORF 096.ng>:

a096.pep

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHAARFRTDCLRAANRQFAHQAFFGFG

```


299

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK
101 PFGNDFAXES VSILRKRFSD GLFL*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHA	AFFRTDCLRAANRQFAHQAFFGFGQIFRRTLIN				
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHA	AFFRTDCLRAANRQFAHQAFFGFGQIFRRTLIN				
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPFVQDGAGIFAAADKTFGNDFAXEGVSILRKRFSD					
a096	GVVAVVLGFVVIKLRGDDVYAGQAFVQHRAGIFAAADKPFGNDFAXESVSILRKRFSD					
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

1	ATGGATATTT	CAAAACAAAC	ATTGCTGGAT	AGGGTTTTTA	ACCTGAAGGC
51	AAACGGTACG	ACGGTACGTA	CCGAGTTGAT	GGCGGGTTTG	ACGACCTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAATC	CCCTGATTTT	GGGCGAGACC
151	GGAATGGATA	TGGGGGCGGT	ATTCGTCGCT	ACCTGTATCG	CATCCGCCAT
201	CGGCTGTTTT	GTCATGGGTT	TTATCGGCAA	CTATCCGATT	GCGCTTGCCC
251	CGGGGATGGG	GCTGAATGCC	TATTTACACT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCCCT	GGCAGGTGGC	GTTGGGTGCG	GTGTTTCAAT	CCGGTCTGAT
351	TTTCATCCTG	TTTCACTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCGTATGGG	TTTGAAAATG	TCGATTGCGG	CCGGTATCCG	TTTGTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCGGC	TTGGGCGATA	TTTCATCAGC	CAGCGCACTG	TTGGCATTGT
551	TCGGTTTTGT	CATGGTGGTC	GTATTGGGGT	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTCTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAGTTT	CACGGCGTGG	TCGGCGAAGT	ACCGGGCATT	GCGCCGACCT
701	TTATGCAGAT	GGATTTTAAA	GGTCTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATTTGTTC	GACAGTACCG	GAACGCTGGT
801	CGGCGTATCC	CACCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TGGCGTGTCT	GATGTTCTCC	CCATTGGCGA	AAAGTGTTC	GGTATTTGCC
1051	ACCGCGCCCG	CACCTGCTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG
1101	GGACATTGAT	TGGGACGATA	TGACTGAAGC	CGCGCCCGCG	TTCTTGACCA
1151	TTGTCTTCAT	GCCGTTTACC	TATTCGATTG	CAGACGGCAT	CGCCTTCGGC
1201	TTTCATCAGT	ATGCCGTGGT	CAAACCTTTG	TGTCGCCGGA	CTGGGGACGT
1251	GCCGCCTATG	GTATGGGTG	TTGCCGTATT	GTGGGCATTG	AAATTCTGGT
1301	ATTTGGGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

1	MDISKQTLTD	RVFNLKANGT	TVRTELMAGL	TTFLTMCIYV	IVNPLILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFIGNYPI	ALAPGMGLNA	YFTFAVVKGM
101	GVPWQVALGA	VFISGLIFIL	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL	LALFGFVMV	VLGYFRVQGA
201	IIITILTITV	IASLMGLNEF	HGVVGEVPGI	APTFMQMDFK	GLFTVSMVSV
251	IFVFFLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSSSTPYV	ESAAGVSAGG	RTGLTAVTVG	VLMLACLMFS	PLAKSVPVFA
351	TAPALLYVGT	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG

m097 . seq	1	51	101	151	201	251	301	351	401	451	501	551	601	651	701	751	801	851	901	951	1001	1051	1101	1151	1201	1251	1301
	ATGGACACTT	CAAACAAC	ACTGTTGGAC	GGGATTTTTTA	AGCTGAAGGC																						
	AAACGGTACK	ACGGTGCCTA	CCGAGTTGAT	GGCGGGTTTG	ACAACTTTTTT																						
	TGACGATGTG	CTACATCGTT	ATCGTCAACC	CTCyGATTTT	GGCGGAGACC																						
	GGCATGGATA	TGGGGGCGGT	ATTCGTCGCT	ACCTGTATCG	CGTCTGCCAT																						
	CGGCTGTTTT	TGTATGGGTT	TTGTCGGCAA	CTATCCGATT	GCACTCGCAC																						
	CGGGATGGG	GCTGAATGCC	TATTTACCT	TTGCCGTCGT	TAAGGGTATG																						
	GGCGTGCCTT	GGCAGGTTGC	GTTGGGTGCG	GTGTTTCATCT	CCGGTCTGAT																						
	TTTTATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC																						
	TGCCTATGGG	TTTGA AAAATG	TCGATTGCTG	CCGGTATCGG	TTTGT TTTTGT																						
	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTGTCCA	ATCCGGCAAC																						
	CTTGGTCCGT	TTGGGCGATA	TTTCATCAGC	GTCCGCGTTG	TTGGCATTGT																						
	TCGGT TTTGC	TATGGTGCTC	GTATTGGGAC	ATTTCCGCGT	TCAAGGCGCA																						
	ATCATCATCA	CATCTTGAC	CATTACCGTC	ATTGCCAGCC	TGATGGGTTT																						
	GAATGAATTT	CACGGCATCA	TCGGCGAAGT	ACCGAGCATT	GCGCCGACTT																						
	TTATGCAGAT	GGATTTTGAA	GGCCTGTTTA	CCGTCAGCAT	GGTCAGTGTG																						
	ATTTTCGTCT	TCTTCTTGGT	CGATCTATTT	GACAGTACCG	GAACGCTGGT																						
	CGGCATATCC	CACCGTGCCG	GGCTGCTGGT	GGACGGTAAG	CTGCCCGGCC																						
	TGAAACGCGC	ACTGCTTGCA	GACTCTACC	CCATTGTGGC	AGGTGCGGT																						
	TTGGGTACTT	CTTCCACAC	GCTTATGTG	GAAAGCGCGG	CGGGCGTATC																						
	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC																						
	TCGCCTGCCT	GATGTTTTCA	CCTTTGGCGA	AAAGTGTTCC	CGCTTTTGCC																						
	ACCGCGCCCG	CCCTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG				</																		

This corresponds to the amino acid sequence <SEQ ID 342; ORF 097>:

```
m097.pep
1  MDTSKQTLTD GIFKLKANGT TVRTELMAGL TTFLTMCIYI IVNPXILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYPI ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFE GLFTVSMVSV
251 IFVFLLVDLF DSTGTLVGIS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng) from *N. gonorrhoeae*:

m097/g097						
	10	20	30	40	50	60
m097.pep	MDTSKQTLLEDGIFKLKANGTTVRTELMAGLTTFLTMCIYIVIVNPXILGETGMDMGAVFVA					
	::					
g097	MDISKQTLLEDRVFNLKANGTTVRTELMAGLTTFLTMCIYIVIVNPLILGETGMDMGAVFVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m097.pep	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	:					
g097	TCIASAIGCFVMGFIGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
	130	140	150	160	170	180

301

m097.pep	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
g097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
	130 140 150 160 170 180
m097.pep	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTQMDFE
g097	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGVVGEVPGIAPTQMDFK
	190 200 210 220 230 240
m097.pep	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA
g097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGVS HRAGLLVDGKLPRLKRALLADSTAIVAGAA
	250 260 270 280 290 300
m097.pep	LGTSSSTTPYVESAAAGVSAGGRTGLTAVTVGVMLACLMSPLAKSVPAFATAPALLYVGT
g097	LGTSSSTTPYVESAAAGVSAGGRTGLTAVTVGVMLACLMSPLAKSVPVFATAPALLYVGT
	310 320 330 340 350 360
m097.pep	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPMM
g097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTGDVPMM
	370 380 390 400 410 420
m097.pep	VWIVAVLWALKFWYLGX
g097	VWVVAVLWALKFWYLGX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

1	ATGGACACTT	CAAAACAAAC	ACTGTTGGAC	GGGATTTT	AGCTGAAGGC
51	AAACGGTACG	ACGGTGCCTA	CCGAGTTGAT	GGCGGGTTTG	ACAACTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAACC	CTCTGATTTT	GGGCGAGACC
151	GGCATGGATA	TGGGGGCGGT	ATTCGTCGCT	ACCTGTATCG	CGTCTGCCAT
201	CGGCTGTTTT	GTTATGGGTT	TTGTCGGCAA	CTATCCGATT	GCACTCGCAC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCTT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCTTT	GGCAGGTTGC	GTGGGTGCG	GTGTTTCATCT	CCGGTCTGAT
351	TTTCATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAAATG	TCGATTGCTG	CCGGTATCGG	TTTGTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTTCGG	TTGGGCGATA	TTTCATCAGC	GTCCGCGTTG	TTGGCACTGT
551	TCCGTTTTGC	CATGGTGGTC	GTATTGGGAC	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTTTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAATTT	CACGGCATCA	TCGGCGAAGT	GCCGAGCATT	GCGCCGACTT
701	TTATGCAGAT	GGATTTTAAA	GGGTTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TTTTCCTAGT	CGATCTGTTC	GACAGTACCG	GAACACTGGT
801	CGGTGTATCG	CATCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CTATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGTGCGG	CGGGCGTATC
951	GGCAGGCGGG	CGGACAGGTC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TCGCCTGCCT	GATGTTTTCA	CCTTTGGCGA	AAAGTGTTC	CGCTTTTGCC
1051	ACCGCGCCCG	CCCTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCAG
1101	GGACATCGAT	TGGGACGATA	TGACGGAAGC	CGCACCGCA	TTCCTGACCA
1151	TTGTCTTCAT	GCCGTTTACC	TATTCGATTG	CAGACGGCAT	CGCTTTCGGC
1201	TTCATCAGTT	ATGCCGTGGT	TAAACTTTTA	TGCCCGCGCA	CCAAAGACGT
1251	TCCGCCTATG	GTATGGATTG	TTGCCGTATT	GTGGGCACTG	AAATTCTGGT

302

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 344; ORF 097.a>:

a097.pep

```

1  MDTSKQTLTD GIFKLKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVP PM VWIVAVLWAL KFWYLG*

```

m097/a097 99.3% identity in 436 aa overlap

	10	20	30	40	50	60
m097.pep	MDTSKQTLTDGIFKLKANGTTVRTELMAGLTTFLTMCYIVIVNPNXILGETGMDMGAVFVA					
a097	MDTSKQTLTDGIFKLKANGTTVRTELMAGLTTFLTMCYIVIVNPLILGETGMDMGAVFVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m097.pep	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
a097	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m097.pep	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
a097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m097.pep	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFE					
a097	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m097.pep	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA					
a097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGVS HRAGLLVDGKLPRLKRALLADSTAIVAGAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m097.pep	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVLMACLMFSPLAKSVPAFATAPALLYVGT					
a097	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVLMACLMFSPLAKSVPAFATAPALLYVGT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m097.pep	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVP PM					
a097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVP PM					
	370	380	390	400	410	420
	430					
m097.pep	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 345>:

```
g098.seq
  1 ATGACCGCCG ACGGTCTCTT CGTCGCTTTC AACTTCAATA CGTTTGCCGT
 51 TGTGCGAATA TTGATACCAG TACAGCAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTCGG CGATGTCGCG CGCTTCGCTG TCGGGATGGC TTTCGCGTTC
151 GGGATGAACG CAGCCGAGCA TGGACACGCC GGTACGCATC ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAAGTG TGCGACTTCT TCAAACCTCGC
351 ATTTTGTGTC CAAATTAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

```
g098.pep
  1 MTADGLFVAF NFNTFAVVRI LIPVQDAAQ AGDQFVGDDVA RFAVGMAFAF
 51 GMNAAEHGHA GTHVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV CDFKLAFLC QIRMS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

```
m098.seq
  1 ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
 51 TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTCGG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GGCGACTTCT TCAAACCTCGC
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

```
m098.pep
  1 MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
 51 RMNAAQHGYA GTHVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFKLAFLC QIRMS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

```
m098/g098

      10      20      30      40      50      60
m098.pep MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g098      MTADGLFVAFNFNTFAVVRI LIPVQDAAQAGDQFVGDDVARFAVGMAFAFGMNAAEHGHA
      10      20      30      40      50      60

      70      80      90     100     110     120
m098.pep GTHVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFKLAFLC
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g098      GTHVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV CDFKLAFLC
      70      80      90     100     110     120

m098.pep QIRMSX
|||
g098      QIRMSX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

```
a098.seq
  1 ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
 51 TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
```

304

```

101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTTAA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GGCGACTTCT TCAAACCTCG
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVR I LIPVQEDAAE AGDQFVG DVA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMG M CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

```

              10      20      30      40      50      60
m098.pep      MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVG DVARFTFRMAFTFRMNAAQHGYA
              |||
a098           MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVG DVARFTFRMAFTFRMNAAQHGYA
              10      20      30      40      50      60

              70      80      90     100     110     120
m098.pep      GTHYVHRMGMC RQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC
              |||
a098           GTHYVHRMGMC RQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC
              70      80      90     100     110     120

m098.pep      QIRMSX
              |||||
a098           QIRMSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGTTG
101 CACTGACCGA ATTCTTGCCT AAAGAGCGCG TGGTCGGGGC GTTTGTGCGAA
151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCGGTTTATC CGCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTGTT GCGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTTGTCT CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcgG CGCGCTcgac CCGAAAATCC AACAAAGAAAT
801 CATCGACCGC GAttgtacg cCACCGCCGT ATTGTCAGGC AACC GCAACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCTT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCCGTCC GCCCTATTGG GAAGGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCCGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCGA TTTTGGCCGG cagTGCgca ggtgaATATT

```

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1301 TGGCGAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GGCGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTCACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KROAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEEPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQEIIIDR DLYATAVLSG NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRRPYPW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGQ GSSRDWAAKG VRLAGVEAIA AEGFERIHRT
551 NLIGMGVLPL QFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEEALVY EAGGVLRFA QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGGCAGG CGGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCCGTTTATC CTCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCAGAC
451 GCCGATTTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCCGACGGCT CGGTCATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCAGCG
601 AATGCCAACC GTCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTTGTACG CCACCGCCGT ATTATCAGGC AACCAGCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTCTT CGCTTCGCCT
901 CCGTTGGTCG TTGCCCTACG GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGGCCGT CAGTGCCGCA GGCGAGTATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGCAG CAAGGCTCGT
1451 TCGCCCGCGT CGAACCCGAA GGCGAAACCA TCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

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1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGCGC GCGTGTGCA ACGGTTTGA CAGGATTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
  1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
 51  FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101  VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151  ADLAAKGLAK PYEEPDQGM PDGSVIIAAI TSCTNTSNPR NVVAAALLAR
201  NANRLGLKRK PWVKSSFAPG SKVAEIIYLKE AGLLPEMEKL GFGIVAFAC
251  TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFASP
301  PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351  PQQFRDVYVP MFDTGTAQKA PSPLYDWRPM STYIRPPYVW EGALAGERTL
401  RGMRLAILP DNITDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451  RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501  ETYMNKQPL IIIAGADYQG GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551  NLIGMGVLPL QFKPDTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601  ETVEVPVTC LDIAEEVLVY EAGGVLQRFQ QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

m099.pep	10	20	30	40	50	60
	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
	IGDRATISNMTPEFGATAAMFAIDEQTIDYKLKLTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYKLKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEEPDQGMPSVIIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEEPDQGMPSVIIAAI					
	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
	GFGIVAFACCTTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFASP					
g099	GFGIVAFACCTTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFASP					
	250	260	270	280	290	300
	310	320	330	340	350	360

307

m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVYVP
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIWPTDEEIDAIVAEYVKPQQFRDIYIP
	310 320 330 340 350 360
m099.pep	MFDTGTAQKAPSPLYDWRPMSYIRRPYWEGALAGERTLRGMRPLAILPDNITTDHLSP
g099	MSDTGTAQKAPSPLYDWRPMSYIRRPYWEGALAGERTLRGMRPPAILPDNITTDHISP
	370 380 390 400 410 420
m099.pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
	430 440 450 460 470 480
m099.pep	QGSFARVEPEGETMRMWEAIETYMNKQPLIIIAGADYGQGSSRDWAAKGVRLAGVEAIV
g099	QGSLARVEPEGQTRMWEAIETYMNKQPLIIIAGADYGQGSSRDWAAKGVRLAGVEAIA
	490 500 510 520 530 540
m099.pep	AEGFERIHRTNLIGMVLPLQFKPDTNRHTLQLDGTETDYDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHRTNLIGMVLPLQFKPDTNRHTLQLDGTETDYDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099.pep	ETVEVPVTCCLDTAEVVLVYEAGGVLQRFAQDFLEGNAAX
g099	ETVEVPVTCRPDTAEELVYEAGGVLQRFAQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099.seq

1	ATGCTGGGAC	GCGCGTCCAT	GATGCGCCTG	CCCGATATTG	TCGGCGTTGA
51	GCTGAACGGC	AAACGGAAGG	CGGGCATTAC	GGCGACGGAT	ATTGTGTTGG
101	CACTGACCGA	GTTTCTGCGC	AAAGAACGCG	TGGTCGGGGC	GTTTGTGCGAA
151	TTCTTCGGCG	AGGGCGCGAG	AAGCCTGTCT	ATCGGCGACC	GCGCGACCAT
201	TTCCAACATG	ACGCCGAGT	TCGGCGCGAC	TGCCGCGATG	TCGCTATTG
251	ATGAGCAAAC	CATTGATTAT	TTGAACTGA	CCGGACGCGA	CGACGCGCAG
301	GTGAAATTGG	TGGAAACCTA	CGCCAAAACC	GCAGGCTTGT	GGGAGATGC
351	CTTGAAAACC	GCCGTTTATC	CGCGCGTTTT	GAAATTTGAT	TTGAGCAGCG
401	TAACGCGCAA	TATGGCAGGC	CCGAGCAACC	CGCACGCGCG	TTTTGCGACC
451	GCCGATTTGG	CCGGCAAAGG	CTTGGCTAAA	CCTTACGAAG	AGCCTTCAGA
501	CGGCCAAATG	CCTGACGGTG	CAGTGATTAT	TGCCGCGATT	ACTTCCTGTA
551	CCAATACTTC	CAATCCGCGC	AACGTTGTG	CCGCCGCGCT	GTTGGCACGC
601	AATGCCAACC	GCCTCGGCTT	GCAACGCAAA	CCTTGGGTGA	AATCTTCGTT
651	TGCCCCGGGT	TCAAAAGTAG	CCGAAATCTA	TTTGAAAGAA	GCAGATCTGC
701	TGCCCCGAAAT	GGAAAACTC	GGCTTCGGTA	TCGTTGCCTT	CGCATGTACC
751	ACCTGTAACG	GCATGAGCGG	CGCGCTGGAT	CCGAAAATCC	AGAAAGAAAT
801	CATCGACCGC	GATTTGTACG	CCACCGCCGT	ATTGTCAGGC	AACCGCAACT
851	TTGACGGCCG	TATCCATCCG	TATGCGAAAC	AGGCTTTCCT	CGCTTCGCCT
901	CCGTTGGTCG	TTGCCACGCG	GCTGGCAGGC	AGCATCCGTT	TCGATATTGA
951	AAACGACGTA	CTCGGCGTTG	CAGACGGCAA	AGAAATCCGC	CTGAAAGACA
1001	TTTGGCCTAC	CGATGAAGAA	ATCGATGCCA	TCGTTGCCGA	ATATGTGAAG
1051	CCGCAGCAAT	TTTCGCGACG	TTATATCCCG	ATGTTGCGACA	CCGGCAGCAGC
1101	GCAAAAAGCA	CCAAGCCCGC	TGTACGACTG	GCGTCCAATG	TCTACCTATA
1151	TCCGCCGCCC	ACCTTACTGG	GAAGGCGCAC	TGGCAGGGGA	ACGCACATTA
1201	AGCGGTATGC	GTCCGCTGGC	GATTTTGCCC	GACAACATCA	CCACCGACCA

```

1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTTCGC
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTCACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTT
1901 TGGAAGGGAA CCGCGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```

1 MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRTISNM TPEFGATAAM FAIDEQIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWVKSSFAPG SKVAEIIYLKE ADLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFLASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVYIP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 SGMRLAILP DNITDHLSP SNAIASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGQ GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551 NLIGMGVLPL QFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLQRF A QDFLEGNA*

```

m099/a099 97.5% identity in 639 aa overlap

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFFGEGARSLS					
a099	MLGRASMMRLPDIVGVELNGKRKAGITATDIVLALTEFLRKERVVGAFVEFFFGEGARSLS					
	10	20	30	40	50	60
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAGLAKPYEPPSDGQMPDGSVIIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAGKGLAKPYEPPSDGQMPDGAIIAAI					
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAGLAKPYEPPSDGQMPDGSVIIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAGKGLAKPYEPPSDGQMPDGAIIAAI					
	130	140	150	160	170	180
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWVKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRKPWVKSSFAPGSKVAEIIYLKEADLLPEMEKL					
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWVKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRKPWVKSSFAPGSKVAEIIYLKEADLLPEMEKL					
	190	200	210	220	230	240
m099.pep	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF L ASP					
a099	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF L ASP					
	250	260	270	280	290	300
m099.pep	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF L ASP					
a099	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF L ASP					
	250	260	270	280	290	300
m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAIVAEYVKPQQFRDVYVP					
a099	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAIVAEYVKPQQFRDVYVP					
	310	320	330	340	350	360

309

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|||||:|||||:|||||:|||||:
a099      PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPTDEEIDAIVAEYVKPQQFRDVIIP
          310      320      330      340      350      360

          370      380      390      400      410      420
m099.pep  MFDGTGAQKAPSPLYDWRPMSTYIRRPYEWEGALAGERTLRGMRPLAILPDNITTDHLSP
          370      380      390      400      410      420
a099      MFDGTGAQKAPSPLYDWRPMSTYIRRPYEWEGALAGERTLSGMRPLAILPDNITTDHLSP
          370      380      390      400      410      420

          430      440      450      460      470      480
m099.pep  SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
          430      440      450      460      470      480
a099      SNAILASSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
          430      440      450      460      470      480

          490      500      510      520      530      540
m099.pep  QGSFARVEPEGETMRMWEAIETYMNRRKQPLIIAGADYGQGSSRDWAAKGVRLAGVEAIV
          490      500      510      520      530      540
a099      QGSLARVEPEGQTMRMWEAIETYMNRRKQPLIIAGADYGQGSSRDWAAKGVRLAGVEAIV
          490      500      510      520      530      540

          550      560      570      580      590      600
m099.pep  AEGFERIHRTNLIGMGVLPLOQFKPDTNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG
          550      560      570      580      590      600
a099      AEGFERIHRTNLIGMGVLPLOQFKPGTNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG
          550      560      570      580      590      600

          610      620      630      640
m099.pep  ETVEVPVTCCLDTAEEVLVYEAGGVLQRFQDFLEGNAAX
          610      620      630      640
a099      ETVEVPITCRLDTAEEVLVYEAGGVLQRFQDFLEGNAAX
          610      620      630      640

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 357>:

g102.seq

```

1   AtgtCCGCCA AAactecgtc gctcttcggc ggcgcgatga Ttatcgccgg
51  gaagggttatc ggcgcAGgta tgttccccc aaacccacgcc aacttggggg
101 acgggttaaat aggtctcgctg attgtgctgc tgtacacctg gtttccattc
151 tcctccggcgc ccctcatgat tttggaagtc aacacccata acCCccgagg
201 ggcaAGtttt gacaccATGg tcAAagacct gctcgGACGc ggctggaaca
251 tcatcaacgg catcgccgtc gctttggTCc tatacggctc gacctacgcg
301 tacatttttag tcggcgggtga cctGACCGCC AAAGGCAtcg GCAgCGCAGT
351 AGGCGGCCAAA ATTTCgctca CCGTCGGACA actcgtcttc tTCGGCATCC
401 TCGCCTTTTG CGTATGGGCA TCCGCACGCT TGGTCGACCG CTTTACCGGC
451 GTCCTCATCG GCGGCATGGT ATTAACCTTT ATTTGGGCAA CCGCGGCCTT
501 GGTTCGCGAT GCCAAACCGT CCGTCTCTT CGACACCCAA GCCCCGCTCG
551 GCACCGGCTA CTGGATTAC GCCGCCACCG CCCTGCCCGT CTGCCTCGCT
601 TCCTTCGGCT TCCACGGCAA CGTTCCAGC CTGCTCAAAT ACTTTAAAGG
651 CGACGcgCc aaagtGgCGA aATCcatctg gGcaggtaca ttggTTGCct
701 tggtaattta cgtccTCTg caaacggcca tCcaaagcaa ccTGCcgcg
751 aacgagttcg cCCCcgtgat tgccgccgag aggcaactCT CCGTCTTgaa
801 tgaaaccctG tccaaattcg cccaaaccgg cgatatggat aAaatattgt
851 ccctatttcc ctacatggca atcgccacct cctttttagg cgTAACctta
901 ggcctgtttg acaacatcgc cgacatcttc aaatggaacg acagtatgtc
951 cgggcggggc accaaaaccg tcgcgctgaa ctctctgccc CCCtgaatt
1001 cctggctgct cctccccacc ggcttcttta ccgccattgg tcgctccggc
1051 ctggcgccaa ccgtctggga ccaagGcatc atccccgcca tgctgctcta
1101 cgtttccccc caaaaaattG gcGcaggcaa gacttataAa gtttaCGGCG
1151 gcttggtgct gatgttagtc ttccttttcg gcatcgccaa catcgccgca
1201 CAGGTATTGA GccaAatgGa ACTcgtCccc GTATTAAAG GATAA

```

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.pep

```

1  MSAKTPSLFG  GAMIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDREFTG
151 VLIGGMVLTF  IWATGGLVAD  AKPSVLFDTQ  APVGTGYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQSVLNETL  SKFAQTGDM  KILSLFPYMA  IATSFLGVTL
301 GLFDNIADIF  KWNDMSMRG  TKTVALNFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGGWLMLV  FLFGIANIAA
401 QVLSQMELVP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGC  GGC CGCATGA  TTATCGCCGG
51  CACGGTCATC  GGC CGCAGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCCAGCG  GCCTGATGAT  TTGGAAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGCGCGCGA  CCTGACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGCGAC  GTTCACTCA  CCGTCGGACA  ACTCGTCTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTCGACCG  CTTACCGGCG
451 GTCCTTATCG  GCGGCATGGT  ATTGACCTTT  ATTTGGGCGG  CCGGCGGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCCTCTT  CGATACCCAA  GCCCCGCGCG
551 GCACAAACTA  CTGGATTAC  GCCGCCACCG  CCCTGCCCGT  CTGCCTCGCT
601 TCCTTCGGCT  TCCACGGCAA  CGTCTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651 CGACGCGCCC  AAAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCTCTGG  CAAACCGCCA  TCCAAGGCAA  CCTGCCGCGC
751 AACGAGTTCG  CCCCCGTCAT  CGCCGCCGAA  GGGCAAGTCT  CGTCTCAT
801 CGAAACCTCG  TCCAAATTCG  CCCAAACCGG  CAATATGGAC  AAAATATTGT
851 CCCTGTTTTC  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCGACCC  AAAACCGCG  CGCTGACCTT  CCTGCCGCCC  CTGATTTCCT
1001 GCCTGCTCTT  CCCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 CGGCGAACCG  TCTGGACAGG  CATCATCCCC  GCCATGCTGC  TCTACCGTTC
1101 GCGCAAAAAA  TTCGGCGCAG  GCAAAACCTA  TAAAGTTTAC  GCGCGCTTGT
1151 GGCTGATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTGAGCC  AAATGGAAC  CGTCCCCGTA  TTAAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFSM
51  LSSGLMILEV  NTHYPHGASF  DTMVKDLLGR  GWNIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDREFTG
151 VLIGGMVLTF  IWAAGGLIAD  AKPSVLFDTQ  APAGTNYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWTGT  LIALVIYVLW  QTAIQGNLPR
251 NEFAPVIAAE  QQSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSFLGVTL
301 GLFDYIADIF  KWNDISISRT  KTAALTFLEP  LISCLLFTPG  FVTAIGYVGL
351 AATVWTGIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAQ
401 VLSQMELVPV  FRK*

```

m102/g102 86.0% identity in 415 aa overlap

```

          10      20      30      40      50      60
m102.pep  MPNKTPSLFGGAMIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g102       MSAKTPSLFGGAMIAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFPFSSGALMILEV
          10      20      30      40      50      60

          70      80      90     100     110     120
m102.pep  NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g102       NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK
          70      80      90     100     110     120

          130     140     150     160     170     180
m102.pep  VSLTVGQLVFFFGILAFVCWASARLVDREFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ
          : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g102       ISLTVGQLVFFFGILAFVCWASARLVDREFTGVLIGGMVLTFIWAATGGLVADAKPSVLFDTQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m102.pep  APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTIALVIYVLW

```

311

```

g102      ||:||:|||||
          APVGTGYWIIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWAGTLVALVIYVLW
          190      200      210      220      230      240

          250      260      270      280      290      300
m102.pep  QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL
          ||||:|||||
g102      QTAIQSNLPRNEFAPVIAAERQLSVLNETLSKFAQTGDMDKILSLFPYMAIATSFLGVTL
          250      260      270      280      290      300

          310      320      330      340      350
m102.pep  GLFDYIADIFKWNDSISGR-TKTAALTFLPPLISCLLFPTGFVTAIGYVGLAATVWT-GI
          |||| |||||
g102      GLFDNIADIFKWNDSMSGRGRTKTVALNFLPPLISWLLPTGFFTAIGASGLAATVWDQGI
          310      320      330      340      350      360

          360      370      380      390      400      410
m102.pep  IPAMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIVNIAAQVLSQMELVPVFKGX
          ||||| | :|||
g102      IPAMLLYVSPQKIGAGKTYKVYGGGLWML-VFLFGIANIAAQVLSQMELVPVFKGX
          370      380      390      400      410

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 361>:

a102.seq

```

1   ATGCCACCA AAACCCCTTC ACTGTTCCGC GCGCGATGA TTATCGCCGG
51  CACGNTCATC GCGCAGGTA TGCTCGCCAA CCCGACCGCC ACATCCGGCG
101 TATGGTTTAC CGGCTCGCTG GCCGTGTTGC TGTACACCTG GTTTTCCATG
151 CTCTCCAGCG GCCTGATGAT TTTGGAAGTC AACACCCACT ACCCCACGCG
201 CGCGANCTTC GACACCATGG TTAAAGACCT GCTCGGACGG AGCTGGAACA
251 TCATCAACGG CATCGCCGTC GCCTTCGTTT TATACCTGCT TACTTACGCT
301 TATATCTTCG TCGGCGGCGA CCTGACCGCC AAAGGCTTAG GCAGCGCGGC
351 AGGCGGCAAT GTTTCACTCA CCGTCGGACA ACTCGTCTTC TTCGGCATTC
401 TCGCCTTTTG CGTATGGGCA TCCGCACGCT TGGTCGACCG ATTCACCAGC
451 GTCCTCATCG GCGGCATGGT ATTAACCTTT ATTTGGGCAA CCGCGGCCT
501 GATTGCCGAT GCCAACTGC CCGTCCTCTT CGACACCCAA GCCCCTACCG
551 GCACCAACTA CTGGATTTAT GTCGCCACCG CCCTGCCCCT GTGCCTTGCG
601 TCATTCGGTT TCCACGGCAA CGTCTCCAGC CTGCTCAAAT ACTTTAAAGG
651 CGACGCGCCC AAAGTGCTA AATCCATCTG GACGGGCACA CTGATTGCGC
701 TGGAATTTA CGTCTCTTGG CAAACCGCCA TCCAANGCAA CCTGCCGCGC
751 AACGAGTTCG CCCCCGTGAT TGCCGCGCAA GGGCAAGTCT CCGTCNTGAT
801 TGAACCCCTG TCCAAATTCG CCAAACCGG CAATATGGAC AAAATATTGT
851 CCCTGTTTTT CTATATGGCG ATCGCCACCT CGTTTTTtag CGTAACGCTC
901 GGA CTCTTCG ACTACATCGC CGACATCTTC AAATGGAACG ACAGCGTGTC
951 CGGCCGCACC AAAACCGCCG CGCTGACCTT CCTGCCGCTT NTAATTTCTT
1001 CCCTGCTCTT CCCCACCGGC TTTGTTACCG CCATCGGNTA CGTCGGCCTG
1051 GCGGCAACCG TCTGGACAGG CATCATCCCC GCCATGCTGC TNTACCGTTC
1101 GCGCAAAAAA TTCGGCGCAG GCAAAACCTA TAAAGTTTAC GCGGCGTTGT
1151 GGCTGATGGT TTGGGTCTTC CTTTTCGGCA TCNTCAACAT CGCCGCACAN
1201 GTATTGAGCC AAATGGAAC TTTAAAGGAT AA
1202

```

This corresponds to the amino acid sequence <SEQ ID 362; ORF 102.a>:

a102.pep

```

1   MPTKTPSLFG GAMIIAGTXI GAGMLANPTA TSGVWFTGSL AVLLYTWFSM
51  LSSGLMILEV NTHYPHGAXF DTMVKDLLGR SWNIINGIAV AFVLYLLTYA
101 YIFVGGDLTA KGLGSAAGGN VSLTVGQLVF FGILAFVCWA SARLVDRTFS
151 VLIGGMVLTF IWATGGLIAD AKLPVLFDTQ APTGTNYWIY VATALPVCCLA
201 SFGFHGNVSS LLKYFKGDAP KVAKSIWTGT LIALVIYVLW QTAIQXNLPR
251 NEFAPVIAAE GOVSVXIETL SKFAQTGNMD KILSLFSYMA IATSFLGVTL
301 GLFDYIADIF KWNDSVSGRT KTAALTFLPP XISCLLFPTG FVTAIGYVGL
351 AATVWTGIIP AMLLYRSRKK FGAGKTYKVY GGLWLMVWVF LFGIXNIAAX
401 VLSQMELVPV FKG*

```

m102 / a102 95.9% identity in 413 aa overlap

312

m102.pep	10	20	30	40	50	60
	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
a102	MPTKTPSLFGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
	10	20	30	40	50	60
m102.pep	70	80	90	100	110	120
	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFCVWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFCVWASARLVDRFTSVLIGGMVLTFIWATGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
	190	200	210	220	230	240
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVLIELTSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSXLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
	250	260	270	280	290	300
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDISGRKTAAALFLPPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDISVGRKTAAALFLPPXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIVNIAAQVLSQMELVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIXNIAAXVLSQMELVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

1	Atgtccgcag	aaaCATACAc	acAAAAtcggc	tGGgtaggct	taggGcaaat
51	gGgtctgcct	atgGTAACGC	GGCTCTTGGA	CGGCGGCATC	GAAGTCGGCG
101	TATACAACCG	CTCGCCCGAC	AAAAC TGCCC	CCATCTCcgC	CAAAGGAGCA
151	AAAGTTTACG	GCagcACCGC	CGAACTCGTC	CGCGCCTGCC	CCGTCATTTT
201	CCTGATGGTT	TCCGACTATG	CCGCCGTGTG	CGACATCCTG	AACGGAGTCC
251	GCGACGGATT	GGCCGGCAAA	ATCATCGTCA	ACATGAGCAC	CATCTCCCCG
301	ACCGAAAACC	TCGCCGTCAA	AGCACTTGTC	GAAGCCGCAG	GCGGACAGTT
351	TGCCGAAGCA	CCCGTTTCCG	GATCGGTCGG	ACCCGCCACC	AACGGCACAC
401	TGCTGATTCT	GTTCGGCGGC	AGCGAAGCCG	TTTTAAACCC	GCTGCAAAAA
451	ATATTTTCCC	TTGTCGGCAA	AAAAACCTTC	CATTTTCGGCG	ATGTCGGCAA
501	AGGCTCGGGC	GCGAAACTCG	TCTTGAATC	GCTCTTAGGC	ATTTTCGGCG
551	AAGCGTACAG	CGAAGCGATG	CTGATGGCGC	GGCAGTTCGG	CATCGATACC
601	GACACCATCG	TCGAAGCCAT	CGGCGGCTCG	GCAATGGACT	CGCCTATTGT
651	TCAAACAAAA	AAATCACTAT	GGGCAAAACG	TGAGTTCCCC	CCTGCCTTTG
701	CACTCAAAACA	CGCTTCCAAA	GAcctTAACC	TCGcgcgcAA	AGAGCTTGAA
751	CAGGCAGGCA	ACACCCTGCC	CGCCGTCGAA	ACCGTTGCTG	CCAGCTACCG
801	CAAAGCAGTT	GAAGCCGGCT	ACGGCGAACA	GGACGTTTCC	GGCGTTTACC
851	TGAAATTGGC	AGAACACTGA			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

Computer analysis of this amino acid sequence gave the following results:

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
g105.pep		MSAETYTQIGWVGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAELV					
m105		MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
		10	20	30	40	50	60
		70	80	90	100	110	120
g105.pep		RACPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGQFAEA					
m105		RDYPVIFLMVSDYAAVCDILNGVRDGLAGXIIIVNMSTISPTKLAVALVEAQR-QFAEA					
		70	80	90	100	110	
		130	140	150	160	170	180
g105.pep		PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSAGKLVLNSSLG					
m105		PVSGSVGPATNGTLLILFGGSEPFXTCKKYPFSSAKKP-SISAMSAKVRARNSSXSTRSW					
		120	130	140	150	160	170

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	:	:				
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXXFALKHASK					
	180	190	200	210	220	230
	250	260	270	280	289	
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSQVYLKLAEH					
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSQVYLKLAEH					
	240	250	260	270	280	

a105.seq

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

1	MSANEYTTQIG	WIGLQMGPL	MVTRLLDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYGNTAELV	RDYPIVIFLM	<u>SDYA</u> <u>AVCDIL</u>	NGVRDGLAGK	IIVNMSTISP
101	TENLAVKLAV	EAAQGVGFMEA	PVSGSVGPAT	NGRTLILFGG	SEAVLNPLQK
151	IFSLVGKKT	HFGDVGKGS	AKLVLSNLLG	IFGEAYSEAM	LMARQFGIDT
201	DTIVEAIGGS	AMDSPMFQTK	KSLWANREFP	PAFLKHKASK	DNLNVLVKE
251	QAGNTLPAVE	TVAASYRKAV	EAGYGEODVS	GYALKLAEH*	

		10	20	30	40	50	60
m105.pep		MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
		:					
a105		MSANEYTQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
		10	20	30	40	50	60
		70	80	90	100	110	119
m105.pep		RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAG-QFAEA					
a105		RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAGQFAEA					
		70	80	90	100	110	120
	120	130	140	150	160	170	179
m105.pep		PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKT FHF GDVGKGS GAKLVLN SLLG					
a105		PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKT FHF GDVGKGS GAKLVLN SLLG					
		130	140	150	160	170	180
	180	190	200	210	220	230	

315

```

m105.pep    IFGDV-QRXMLMARQFGIDTDIVEAIGDSAMDSPMFQTKKSLWANREFPXAFALKHASK
|||::: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190      200      210      220      230      240

m105.pep    240      250      260      270      280
DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a105        250      260      270      280      290
DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

g105-1.seq

```

1  ATGTCCGCAG AAACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACC GC AACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

g105-1.pep

```

1  MSAETYTOIG WVGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVGSTAEVLV RACPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLILIFGG SEAVLNPLQK
151 IFSLVGKKTF HFQDVGKGS G AKLVLSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

m105-1.seq

```

1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACC GC AACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGTTCGGGC GCGAAACTCG TCTTGAATC GCTCTGGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGSGACTCG GCAATGGACT CGCCCATGTT
651 CCAAACAAA AAATCCCTGT GGGCAAACCG CGAATTCCTG CCCGCTTCG
701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAACTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

m105-1.pep

```

1  MSANEYAQIG WIGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVGNTAEVLV RDPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```

316

101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
 151 IFSLVGKKTFF HFGDVGKGS AKLVLSLLG IFGEAYSEXM LMARQFGIDT
 201 DTIVEAIGDS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

m105-1/g105-1 96.9% identity in 289 aa overlap

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLQMGMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
g105-1	MSAETYTQIGWVGLQMGMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAELV					
	10	20	30	40	50	60
m105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAGGQFAEA					
g105-1	RACPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
m105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAGGQFAEA					
g105-1	RACPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
m105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVLSLLG					
g105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVLSLLG					
	130	140	150	160	170	180
m105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVLSLLG					
g105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVLSLLG					
	130	140	150	160	170	180
m105-1.pep	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
g105-1	IFGEAYSEAMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	190	200	210	220	230	240
m105-1.pep	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
g105-1	IFGEAYSEAMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	190	200	210	220	230	240
m105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX					
g105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

a105-1.seq

1 ATGTCCGCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
 51 GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGCGCGCATC GAAGTCGGCG
 101 TATACAACCG CTCGCCGAC AAAACTGCC CCATCTCCGC CAAAGGCGCA
 151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
 201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
 251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG
 301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAG GCGGACAGTT
 351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
 401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
 451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
 501 AGGTTCCGGG GCGAAACTCG TCTTGAACCT GCTCTTGGGC ATTTTCCGGC
 551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
 601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT
 651 CCAAACCAAA AAATCCCTGT GGGCAAACCG CGAATTCCCA CCCGCTTCG
 701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
 751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
 801 CAAAGCAGTC GAAGCCGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
 851 TGAAATTGGC AGAACACTGA

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

a105-1.pep

1 MSANEYTQIG WIGLQMGMLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
 51 KVGYNTEALV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
 101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
 151 IFSLVGKKTFF HFGDVGKGS AKLVLSLLG IFGEAYSEAM LMARQFGIDT
 201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

a105-1/m105-1 99.0% identity in 289 aa overlap

	10	20	30	40	50	60
a105-1.pep	MSANEYTQIGWIGLQMGMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					

m105-1	MSANEYAQIGWIGLGQMG LPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGN TAE LV
	10 20 30 40 50 60
a105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
m105-1	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
	70 80 90 100 110 120
a105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSGAKLVLSLLG
m105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSGAKLVLSLLG
	130 140 150 160 170 180
a105-1.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
m105-1	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK
	190 200 210 220 230 240
a105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
m105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
	250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCcttggtta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cccTgtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcg tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1  MVLTFIWATG GLVADAKPSV LFDTQAPVGT GYWIYAATAL PVCLASFGEFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSE LGVTGLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1  ATGGTATTGA CCTTTATTTG GGCGGCCGCG GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGs CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCCA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1  MVLTFIWAAG GLIADAKPSV LFDTQAPAGT NYWIYAXTAL PVCLASFGEFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
 151 IAHLQMERQH LRAAPKPPR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng) from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
g107	MVLTFIWATGGLVADAKPSVLFDTQAPVGTGYWIYAATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	: : : : :					
g107	KGDAPKVAKSIWAGTLVALVIYVLWQTAIQSNLPRNEFAPVIAAERQLSVLNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSF LGVTLGLFDYIA-HLQMERQHLRAAPKPPR					
	: : : : :					
g107	TGDMDKILSLFPYMAIATSF LGVTLGLFDNIAGHLQMERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGCGCAGC CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTTCCCA
551 CCGCTTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTTCG
651 CGCAGGCAAA ACCTATAAAG TTTACGGCGG CTTGTGGCTG ATGGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWATG GLIADAKLPV LFDQTAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGGWL MVWVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
a107	MVLTFIWATGGLIADAKLPVLFDTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
a107						
	70	80	90	100	110	120
	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIAHLQMERQHLRAAPKPPRX					
a107						
	130	140	150	160	170	180
	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL					
	190	200	210	220	230	240
a107	LFPTGFVTAIGYVGLAATVWTGIIIPAMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

g108.seq

1	ATGttgccgg	gCTTCAACCG	GATATTCAaa	cggTTTGCTC	CAACACTCGG
51	AAcggCGCAT	AAAACGCCgc	ccTTCGCGTT	ATCCCGAACG	GGGCGGCTAA
101	TCAGATCCTA	TCGCCATAAA	AGGCGGGGTT	TCAACCGAAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGTCTAT	TTTGCCGGCG	GCAATCTTAC	TCGGCGGGTG
201	CGCCGCCGGC	GGCAACACAT	TCGGCAGCTT	AGACGGCGGC	ACGGGTATGG
251	GTGGCAGCAT	CGTCAAAATG	ACGGTAGAAA	gccAATGCCG	TGCGGAATTG
301	GACAGCGCA	GCGAATGCCG	TTTGACCGCG	CTGGCGATGA	GTGCCGAAAA
351	ACAGGCGGAA	TGGGAAAACA	AGATTTGCGG	CTGCGCTACC	GAAGAAGCAC
401	CTAACCAGCT	GACCGGCAAC	GATGTGATGC	AGATGCTGaa	ccagtccacG
451	CGCaatcagg	cacTtgccgc	CctgaccgTC	AAAacggTT	CcgctgcTT
501	CAaacgcctg	tACCGCTaa			

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

g108.pep

1	MLPGFNRIK	RFAPTLGTAH	KTPPFALSRT	GRLIRSYRHK	RRGFNRKGIE
51	MNKTLILPA	AILLGGCAAG	GNTFGSLDGG	TGMGGSIVKM	TVESQCRAEL
101	DRRSEWRLTA	LAMSAEKQAE	WENKICGCAT	EEAPNQLTGN	DVMQMLNQST
151	RNQALAAALTV	KTVSACFKRL	YR*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

m108.seq

1	ATGTTGCCGG	GCTTCAACCG	GATATTCAAA	CGGTTTGTTT	CAACACTCGG
51	AACGGCGCAT	AAAACGCCGC	CCTTCGCGTT	ATCCCGAACG	GGGCGGCTAA
101	TCAGATTCTA	TCGCCATAAA	AGGCGGGGTT	TCAACCGAAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGTCTAT	TTTGCCGGTG	GCAATCTTAC	TCGGCGGCTG
201	CGCCGCCGGA	GGCGGTAACA	CATTCCGGCAG	CTTAGACGGT	GGCACAGGCA
251	TGGGCGGCAG	CATCGTCAAA	ATGGCGGTTG	GGAGCCAATG	CCGTGCGGAA
301	TTGGACAAAC	GCAGCGAATG	GCGTTTGACC	GCGCTGGCGA	TGAGTGCCGA
351	AAAACAGGCG	GAGTGGGAAA	ACAAGATTG	CGCTTGCGTC	GCCCAAGAAG
401	CACCCGAACG	GATGACCGGC	AACGATGTGA	TGCAGATGCT	GGCTCCGTCC
451	ACGCGCAATC	AGGCACTTGC	CGCCCTGACC	GCCAAAACGG	TTTCCGCCTG
501	CTTCAAACAC	CTGTACCGCT	AA		

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

m108.pep

1	MLPGFNRIK	RFVPTLGTAH	KTPPFALSRT	GRLIRFYRHK	RRGFNRKGIE
51	MNKTLILPV	AILLGGCAAG	GGNTFGSLDG	GTGMGGSIVK	MAVGSQCRAE
101	LDKRSEWRLT	ALAMSAEKQA	EWENKICACV	AQEAPERMTG	NDVMQMLAPS
151	TRNQALAAAL	AKTVSACFKH	LYR*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108

	10	20	30	40	50	60
m108.pep	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKTL	SILPV	:	:	:	:
g108	MLPGFNRIFKRFAPLTGTAKHTPPFALSRTGRLIRS	YRHKRRGFNRKGIEMNKTL	SILPA	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGGNTFGSLDGGTGMGGSIVKMAVG	SQCRAELDKRSEWRLTALAMSAEKQA	:	:	:	:
g108	AILLGGCAAGG-NTFGSLDGGTGMGGSIVKMTVES	SQCRAELDRRSEWRLTALAMSAEKQA	:	:	:	:
	70	80	90	100	110	
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGNQDMQLAPSTRNQALAALTAKTVSACFKHLYRX	:	:	:	:	:
g108	EWENKICGCATEEAPNQLTGNDVMQMLNQSTRNQALAALTVKTVSACFKRLYRX	:	:	:	:	:
	120	130	140	150	160	170

a108.seq

1	ATGTTGCCGG	GCTTCAACCG	GATATTCAA	CGGTTTGTT	CAACACTCGG
51	AACGGCGCAT	AAAACGCCG	CCTTCGCGT	ATCCCGAAC	GGGCGGCTAA
101	TCAGATTCTA	TCGCCATAAA	AGGCGGGGT	TCAACCGAAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGTCTAT	TTTGCCGGTG	GCAATTCTTA	TCGGCGGGTG
201	CGCGCGCGGG	GGCGGTAA	CATTGCGAG	CTTAGACGG	GGCAGAGTA
251	TGGGCGCGAG	CATCGTCAA	ATGGCGGTAG	AAAGCCAATG	CCGTGCGGAA
301	TTGAACAAAC	GCAGCGAATG	GCGTTTGACC	GCGCTGGCGA	TGAGTGCCGA
351	AAAACAGGCG	GAATGGGAAA	ACAAGATTTG	CGCTTGCGTC	GCCCAAGAAG
401	CACCCAACCA	GCTGACCGCG	AACGATGTGA	TGCAGATGCT	GGATCCGTCC
451	ACGCGCAATC	AGGCACTTGC	GC CCTGACC	GCCAAAACGG	TTTCCGCGTG
501	CTTCAAACAC	CTGTACCGCT	AA		

a108.pep

1 MLPGFNRIKF RVVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNKRGIE
51 MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE
101 LNKRSERLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS
151 TRNOALAALT AKTVSACFKH LYS*

m108/a108 96.5% identity in 173 aa overlap

	10	20	30	40	50	60
m108.pep	MLPGFNRI	FKRFVPTL	GTAKHTPP	FALSRTGR	LIRFYRHK	RRGFNKRK
a108	MLPGFNRI	FKRFVPTL	GTAKHTPP	FALSRTGR	LIRFYRHK	RRGFNKRK
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCA	AAGGGNTF	GS�DGGT	GMGGSIV	KMAVGSQC	RAELDKR
a108	AILLGGCA	AAGGGNTF	GS�DGGT	GMGGSIV	KMAVESQC	RAELNKR
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKIC	ACVAQE	APERMT	GNQMLP	STRNQAL	AALTAKT
a108	EWENKIC	ACVAQE	APNQLT	GNQMLP	STRNQAL	AALTAKT
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

g109.seq

```

1  ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGGC
51  AGCCGGTATT GATCGTAGGC GTATGCTTAC CGCTTTTGGA AGCGGGCATG
101 GAAATGACGC GCAAAGGCAA AACCACCCAA TCCGCCGCCA TCGTGGTGT
151 CTCTTCCGTC TGGTCAATCC GGTTTTCGGC TGGGCGTTGA CGATGCTGTT
201 GGATAATTTG GGCTTAATCG GCTGCAAAGA ACGCAGCGCG CAATTAGGTT
251 TTGTCGGACG AGTATTGATA CCCGCGTAG GTTTCTTAAT CTTGTGTGTG
301 GCGATGGGTG CGGTCGGGAT GCTGCCCCGT ATCCCTCCGT TTTTGGAGCA
351 GTTCAAATCT TTGGGCTAG

```

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

g109.pep

```

1  MYRVRVGLS DGLGDLAAGI DRRRLTAFG SHHGNDQRQ NHPIRRHRGV
51  LFRVLPVFG WALTMLLDNL GLIGCKERSA QLGFGVRLI PAVGFLILCV
101  AMGAVGMLPG IPPFLEQFKS LG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 389>:

m109.seq

```

1  ATGTATTATC GCCGGGTTAT GGGGCTATCC GATGGACTTG GCGATTGGC
51  AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CATCGTGGTG TTCTCTTCCG CCTTGTCAT CCGGTTTTCG GCTGGGCGTT
201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAA GAGCGCAGTG
251 CGCAATTAGG TTTCGCCGGA CGCGTGTGA TACCCGAGT AGGTTTCTTG
301 ATCTTGTTG TGGCGATGGG TCGGTCGGG ATGCTGCCCG GTATCCCGCC
351 GTTTTTGGA CACTTCAAAT CTTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 109>:

m109.pep

```

1  MYRVRMGLS DGLGDLAAGI ERSLGRRRIL TAFSGHNGND AQRQNHPIRR
51  HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFAG RVLIPAVGFL
101  ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 109 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 109.ng) from *N. gonorrhoeae*:

m109/g109

	10	20	30	40	50	60
m109.pep	MYRVRMGLSDGLGDLAAGIERSLGRRRILTAFGSHHGNDQRQNHPIRRHRGVLFRLVN					
	: : :					
g109	MYRVRVGLSDGLGDLAAGIDR---RRMLTAFGSHHGNDQRQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	

	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
	:					
g109	PVFGWALTMLLDNLGLIGCKERSAQLGFVGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
	60	70	80	90	100	110

m109.pep	HFKSLGX
	:
g109	QFKSLGX
	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq

```

1  ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGGC
51  AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CACCGTGGTG TTCTCTTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

```

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```

201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAAA GAGCGCAGCG
251 CGCAATTAGG TTTCACCGGA CGCGTATTGA TACCCGTAGT AGGTTTCTTG
301 ATCTTGTTG TGGCGATGGG TGGGTCGGG ATGCTGCCCC GTATCCCGCC
351 GTTTTGGAG CACTTCAAAT CTTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 392; ORF 109>:

a109.pep

```

1 MYYRRVVGLS DGLGDLAAGI ERSLGRRRIL TAFSGSHGND AQRQNHPIRR
51 HRGVLFRVLN PVFGWALTML LDNLGLIGCK ERSAGLGFTG RVLIPVVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

m109/a109 97.6% identity in 126 aa overlap

```

              10      20      30      40      50      60
m109.pep      MYYRRVMGLSDGLGDLAAGIERSLGRRRILTAFGSGHGND AQRQNHPIRRHRGVLFRVLN
              |||||:|||||
a109           MYYRRVVGLSDGLGDLAAGIERSLGRRRILTAFGSGHGND AQRQNHPIRRHRGVLFRVLN
              10      20      30      40      50      60

              70      80      90      100     110     120
m109.pep      PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE
              |||||:|||||
a109           PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLPVVGFLILCVAMGAVGMLPGIPPFLE
              70      80      90      100     110     120

m109.pep      HFKSLGX
              |||||
a109           HFKSLGX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 393>:

g111.seq

```

1 ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAacaaac GCGCAaacg
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CcTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
201 TGATGATGCG CTAAAGAAG TCAACCGGCA GATGtccaCC TACCAGACCG
251 ATTCCGAAAT CAGCCGGTt atacagacan atgctggaga gctcttcgcg
301 tntcatgcag nttctataac tgattccgcc gaagactgtc tgcctaatac
351 gcctatctca tcggcgctct ga

```

This corresponds to the amino acid sequence <SEQ ID 394; ORF 111.ng>:

g111.pep

```

1 MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLQGET MGTITYTVKYL
51 SNNRDKLPSF AKIQKRIDDA LKEVNRQMSY YQTDSEISRF IQTAGELFAH
101 ASITDSAEDC LPNTPISSAL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 395>:

m111.seq

```

1 ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGCGAAACG ATGGGCACGA CCTATAYCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AWAACGCAT
201 CGATGACGCG CTAAAGAAK TCAACCGGyA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301 ATTTCAAGCG ACTTCGACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GGCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCAAG GCCTATTG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA

```


323

```

601 CTGGA AAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAACTCGC TGTTTTCCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAACTGcTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLQGET MGTTYXVKYL
51  SNNRDKLPSP AEIXKRIDDA LKEXNRXMST YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFGPDK SVTREPSPEQ
151 IKQAASYTGI DKIIILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

m111.pep/g111.pep

```

m111.pep      10      20      30      40      50      60
MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSP
|||||||:|:|||||||||||||||||||||||||||||||:|||||||
g111          MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLQGETMGTTYTVKYLSNNRDKLPSP
              10      20      30      40      50      60

m111.pep      70      80      90      100     110     120
AEIXKRIDDALKEXNRXMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH
|:| ||||||| || ||||| ||||||| |:|:
g111          AKIQKRIDDALKEVNRQMSTYQTDSEISRFIQTXAGELFAXHAXSITDSAEDCLPNTPI S
              70      80      90      100     110     120

m111.pep      130     140     150     160     170     180
GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK
g111          SALX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

a111.seq

```

1  ATGCCGTCTG AAACACGCCT GCCGAACTTT ATCCGCACCT TGATATTTGC
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTAAAGAAG TCAACCGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CTTGACACAC GGCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTTCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA
601 CTGGA AAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCTTGCGCG ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA

```

```

801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTTGA AAAAGTCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

```

1 MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLOGET MGTITYTVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTAEAVHLNRLTH GALDVTVGPL VNLWGFDPK SVTREPSPEQ
151 IKQAASYTGI DKIIILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIFLNACSEQTAQTVTLQGETMGTITYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
a111	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVDKVAELEGKYGIQNYLVEIGGELHGKGNARGEPRWIGIEQPNIVQ					
a111	AYLDLSSIAKGFVDKVAELEGKYGIQNYLVEIGGELHGKGNARGEPRWIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNNKRPIHNLASISVVDASAM					
a111	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNNKRPIHNLASISVVDASAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

```

1 ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAaCCG
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
201 TGATGATGCG CTTAAAGAAG TCAACCGCA GATGTCCACC TACCAGACCG

```

325

```

251 ATTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ATTTGCGACA CGTTACCGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACTCAC GGCACACTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGGTTCGG CCCCACAAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGCAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAA GCCTATTGTTG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCggcGAGTT
651 GCACGGCAAA GGCAAAAATG CGCACGGCGA ACCGTGGCGC ATCGGTATAG
701 AGCAACCCAA TATcatccaa ggcggcaata cgcAGattat cgtcccgtg
751 aaCaaccgtt cgcttgccac ttccggcgat taccgtaTTT tccacgtcgA
801 TAAAAACGGC Aaacgccttt cccacATCAT CAATCCCAAC AACAAACGAC
851 CCATCAGcCA CAAcctcgcc tcCATCagCg TGGTCTCAGA CAGTGCAATG
901 ACGGCGGACG GTTTATCCAC AGGATTATTT GTTTTAGGCG AAACCGAAGC
951 CTTAAGGCTG GCAGAACAAG AAAAActCGC TGTTTTCTTA ATTGTCCGGG
1001 ATAAGGACGG CTACCGCACC GCCATGTCTT CCGAATTGTC CAAGCTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 400; ORF 111-1.ng>:

```

g111-1.pep
1  MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLOGET MGTITYVKYL
51  SNNRDKLPSP AKIQKRIDDA LKEVNRQMSY YQTDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASVTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHKG GKNAGPEPWR IGIEQPNIIQ GGNTQIIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVSDSAM
301 TADGLSTGLF VLGETEALRL AEQEKLAFLV IVRDKDGVRT AMSSEFAKLL
351 R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 401>:

```

m111-1.seq
1  ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTGTC
51  CCTGGGTTTC ATCTTCCTGA ACGCCTGTTT GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGCGAAACG ATGGGACAGA CCTATACCGT CAAATACCTT
151 TCAAAAGATG GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAACGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GGCAGCGCTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAAGT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTGTTG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GGCAGCAATA CGCAGATTAT GTTCCCGCTG
751 AACAACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAActCGC TGTTTTCTTG ATTGTCAGGG
1001 ATAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 402; ORF 111-1>:

```

m111-1.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLOGET MGTITYVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASVTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHKG GKNARGEPR IGIEQPNIVQ GGNTQIIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVSADAM
301 TADGLSTGLF VLGETEALKL AEREKLAFLV IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111-1/g111-1 96.6% identity in 351 aa overlap

```

          10      20      30      40      50      60
m111-1.pep MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTITYVKYLSNNRDKLPSP
          |||||:::|||||
g111-1      MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLOGETMGTITYVKYLSNNRDKLPSP

```

326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	: : : :					
g111-1	70	80	90	100	110	120
	AKIQKRIDDALKEVNRQMSTYQTDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSPQIKQAASYTGIDKIILKQKDYASLSKTHPK					
	: : : :					
g111-1	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSPQIKQAASYTGIDKIILQQKDYASLSKTHPK					
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVGDKVAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
	: : : :					
g111-1	190	200	210	220	230	240
	AYLDLSSIAKGFVGDKVAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
m111-1.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAM					
	: : : :					
g111-1	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVSDSAM					
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAFLIVRDKGGYRTAMSSEFEKLLRX					
	: : : :					
g111-1	310	320	330	340	350	
	TADGLSTGLFVLGETEALRLAEQEKLAFLIVRDKDGYRTAMSSEFAKLLRX					

g111-1/p44550

sp|P44550|YOJL_HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR >gi|1074292|pir|C64144
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346
 Score = 349 bits (885), Expect = 2e-95
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEYNRMSTYQ 82
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+
 Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVYKYLDDGSITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRFNQHT-AGKPLRISSDFAHVTAEAVRLNRLTHGALDVTVGPLVNLWGFGPKS 141
 DSE+SRFNQ+T P+ IS+DFA V AEA+RLN++T GALDVTVG+VNLWGFGP+K
 Sbjct: 75 KDSELSRFNQNTQVNTPIEISADFAKVLAEAIRLNKVTEGALDVTVGPPVNLWGFGPEKR 134

Query: 142 VTREPSPEQIKQAASYTGIDKIILKQKDYASLSKTHPKAYLDLSSIAKGFVGDKVAGEL 201
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKGFVG+VA +L
 Sbjct: 135 PEKQPTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVLDLSSIAKGFVG+QVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIVPLNNRSLATSGDY 261
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKPWQIAIEKPTTGERAVEAVIGLNNMGMASGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A
 Sbjct: 255 RIY-FEENGKRFAHEIDPKTGYPIQHHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAVFLIVRDKGGYRTAMSSEFEKL 349
 E+ LAV+LI+R G+ T SS F+KL
 Sbjct: 314 EKNNAVLYLIIRTNDGFTVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTGC
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101  TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151  TCAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201  CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251  ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301  ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG

```

```

351 CCTGACACAC GGC GCGCTGG ACCTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGCGCA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAGCGGCG AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCCGAGA CAGTGCAGTG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAAAGTCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

a111-1.pep

```

1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLOGET MGTITYTVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWFGFDPK SVTREPSPEQ
151 IKQAASVTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVGAE
201 LEKYGIQNYL VEIGGELHKG GKNARGEPWR IGIEQPNIVQ GGNTQIIIVPL
251 NNRLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

	10	20	30	40	50	60
a111-1.pep	MPSETRLPNFIRTLIFALSFIFLNACSEQTAQTVTLOGETMGTITYTVKYLNNRDKLPSP					
m111-1	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTITYTVKYLNNRDKLPSP					
	10	20	30	40	50	60
a111-1.pep	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVHLNRLTH					
m111-1	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
	70	80	90	100	110	120
a111-1.pep	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVHLNRLTH					
m111-1	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
	70	80	90	100	110	120
a111-1.pep	GALDVTVGPLVNLWFGFDPKSVTREPSPEQIKQAASVTGIDKILKQKGDYASLSKTHPK					
m111-1	GALDVTVGPLVNLWFGFDPKSVTREPSPEQIKQAASVTGIDKILKQKGDYASLSKTHPK					
	130	140	150	160	170	180
a111-1.pep	GALDVTVGPLVNLWFGFDPKSVTREPSPEQIKQAASVTGIDKILKQKGDYASLSKTHPK					
m111-1	GALDVTVGPLVNLWFGFDPKSVTREPSPEQIKQAASVTGIDKILKQKGDYASLSKTHPK					
	130	140	150	160	170	180
a111-1.pep	AYLDLSSIAKGFGVDKVGAELEKYGIQNYLVEIGGELHKGKKNARGEPWRIGIEQPNIVQ					
m111-1	AYLDLSSIAKGFGVDKVGAELEKYGIQNYLVEIGGELHKGKKNARGEPWRIGIEQPNIVQ					
	190	200	210	220	230	240
a111-1.pep	AYLDLSSIAKGFGVDKVGAELEKYGIQNYLVEIGGELHKGKKNARGEPWRIGIEQPNIVQ					
m111-1	AYLDLSSIAKGFGVDKVGAELEKYGIQNYLVEIGGELHKGKKNARGEPWRIGIEQPNIVQ					
	190	200	210	220	230	240
a111-1.pep	GGNTQIIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVDASAM					
m111-1	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVDASAM					
	250	260	270	280	290	300
a111-1.pep	GGNTQIIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVDASAM					
m111-1	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVDASAM					
	250	260	270	280	290	300
a111-1.pep	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
m111-1	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

g114.seq

```

1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGACGAG TATGGGGCGG TCAATGTCCG

```

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```

101 TAACGGTAGG TTTGTTTTGT GTTTCATTA ACTTAACAAT ATCTGTCGAA
151 TACGGTCAAA GCGGCTATTT TACCAGAGCC GCCGAATGTA AAACAGGGTG
201 TCAGGGCATC AGCCCGAGCT GCCTGAACGA ACGGACGGTT TGCGAGGTAA
251 CGATAAAATG GTCGAGCAGC GAAACATCAA CCAGCGACAT GGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGGTTTCA GCGAGCCGCC
351 CGGATGGTTG TCGCGATAAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 406; ORF 114.ng>:

```

g114.pep
  1 MASITSPLHG AQECSKTFLL CPPGGTSMGR SMSVTVGLFC VSINLTISVE
 51 YGSGYFTRA AECKTGCGI SPSCLNERTV CEVTIKWSSS ETSTSDMACA
101 SRLVNMSSC EGSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 407>:

```

m114.seq
  1 ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCACAGAG AATGCAGCAA
 51 GACTTTTTTA TGTCCACCGG GCGGGACGAG TATAGGGCGG TCAATGTCGG
101 TAACGGTAGG TTTGTTTTGT GTTTCATTA ACTTAACAAT ATCTGTTGAA
151 TACGGTTGAA GCGGCTATTT TATCAGAGCC GCCGCATGTA AAACAGAGTG
201 TCAGGGCATC AACCCGAGCT GTCTGAACGA ACAGACGCTT TGCGAGGTAA
251 CGATAAAATG GTCGAGCAGC GACACATCGA CCAGCGACAT TGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGTTCTSG GCGAGCCGCC
351 CGGATGGTTG TCGCAATAAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 408; ORF 114>:

```

m114.pep
  1 MASITSPLHG AHRECSKTFLL CPPGGTSIGR SMSVTVGLFC VSINLTISVE
 51 YGXSGYFIRA AACKTECQGI NPSCLNEQTL CXVTIKWSSS DTSTSDIACA
101 SRLVNMSSC EXSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

m114/g114 90.0% identity over a 140 aa overlap

	10	20	30	40	50	60
m114.pep	MASITSPLHGAHRECSKTFLLCPPGGTSIGRSM SVTVGLFCVSVINLTISVEYGXSGYFIRA					
	: : : : : :					
g114	MASITSPLHGAHQECSKTFLLCPPGGTSMGRSM SVTVGLFCVSVINLTISVEYQSGYFTRA					
	10	20	30	40	50	60
m114.pep	AACKTECQGINPSCLEQTLXVTIKWSSSDTSTSDIACASRLVNMSSCEXSGEPPGWL					
	: : : : : :					
g114	AECKTGCGISPSCLNERTVCEVTIKWSSSETSTSDMACASRLVNMSSCEGSGEPPGWL					
	70	80	90	100	110	120
m114.pep	AACKTECQGINPSCLEQTLXVTIKWSSSDTSTSDIACASRLVNMSSCEXSGEPPGWL					
	: : : : : :					
g114	AECKTGCGISPSCLNERTVCEVTIKWSSSETSTSDMACASRLVNMSSCEGSGEPPGWL					
	70	80	90	100	110	120
m114.pep	CAIIRLSAYSSNASLTISRMX					
	: : : : :					
g114	CAIIRLSAYSSNASLTISRMX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 409>:

```

a114.seq
  1 ATGCCGGAGG CAAGCATCGC CTCCATCACT TCGCCGCTGC ACGGGGCGCA
 51 ACAGGAATGC AGCAAGACTT TTTTATGTCC GCCGGGCGGG ACGAGTATGG
101 GCGGTCATC GTCGGTAACG GTAGTTTGT TTTGTGTTT CATTAACTTA
151 ACATATCTG TCGAATACGG TTGAAGCGGC TATTTTATCA GAGCCGCCGC
201 ATGTAAACA GGGTGTCAAG GCATCAGCCC GAGCTGCCTG AACGAACGGA
251 CGGTTTGC GCATTACGATA AAATGGTCGA GCAGCGACAC ATCGACCAGC
301 GACATTGCCT GTGCCAGCCG CCTTGTGAAC ATGATGTCTT CCTGCGAAGG
351 TTCGGGCGAG CCGCCCGGAT GGTGTGCGC GATAATCAGG CTGTCGGCAT
401 ATTCGTCCAA TGCCAGTTTG ACAATTTTAC GGATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1  MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRMSVT VGLFCVSINL
51  TISVEYG*SG YFIRAAACKT GCQGISPSCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCAIIR LSAYSSNASL TISRM*

```

m114/a114 92.9% identity in 140 aa overlap

```

              10      20      30      40      50
m114.pep      MASITSPLHGAHRECSKTFLCPPGGTSIGRMSMSVTVGLFCVSINLTISVEYGXSG
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           MPEASIASITSPLHGAQQECSKTFLCPPGGTSMGRMSMSVTVGLFCVSINLTISVEYGXSG
              10      20      30      40      50      60

              60      70      80      90      100     110
m114.pep      YFIRAAACKTECQGINPSCLNEQTLXVTIKWSSSDTSTSDIACASRLVNMSSCEXSSE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           YFIRAAACKTGCQGISPSCLNERTVCAVTIKWSSSDTSTSDIACASRLVNMSSCEGSSE
              70      80      90      100     110     120

              120     130     140
m114.pep      PPGWLCAIIRLSAYSSNASLTISRMX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           PPGWLCAIIRLSAYSSNASLTISRMX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1  atggtcgacg aactcgacCT GCTGCCCGAT GCCGTCGCCG CCACCCTGCT
51  TGCCGACATC GGACGCTACG TCCCGGATTG GAACCTATTG GTTTCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTGtgga CGAAGTGCAG
151 AAACCTACCC ACTTCGCCCC GGTGGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TGCGGAAAT GCTGCTGGCg atggttaccg
251 Acatccgcgt cgtatTAATC AAACCTGGCGA TGCGTaccg caccCTGcta
301 ttTTtaagCA ACGCCCCCGA CAGCCCTGAA AAACgcgccg TCgcaaaAga
351 aacctTCGAC ATCTTCGCCC CGCTCGCCA CCGCTTGGC GTGTGGCAGC
401 TCAAATGGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGCGAAA TCGCCCTGCT TTTGGACGAA AAACGCACCG AACGCCTCGA
501 ATACATCGAA AACTTCCTCG ATATCCTGCG TACGGAATC AAAAAATACA
551 ATATCCACTT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTTAC
601 AAAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgcccTGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTCG ATACCGTCCC CGAGTGTtAC ACCACGCTGG
701 gcatCGTCCA CAGCCTCTGG CAGCCCATT CCGCGGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaA CGgttATAAA AGtTTGCACA CCGTCATCGT
801 cggcccGGAA gacaaaggtg tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTcAa CgaatTcggT gtcgcccCCC ACTGGCGtta caaagaaggc
901 ggcaaaggcg attccGCcTA cgaacaaAAA ATcgccTggt TGCgccaACT
951 CTTGGACTGG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCGAGCTT TTCAACGACA CGATTtATGT TTTGACCCCG
1051 CACGGCAAAG TCCTCTCTCT GCCAACGGGC GCAACCCCA TCgACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcggCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCCGCTG TCCACCCCGC TCGAAAACGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGGtc aaATCCGGCA AGGCCATCGG caaAATCCG GCCTAcacCC
1301 GCCAGcaaAa cgCgaCACC GTGCGCGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CCAAACCTCAC GCCCAAACCC AACCTGCAAG AGCTTgcccga
1401 aaATCTCGGC taaaaAAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaaatttc caaccgcgcc atCcaaaaag cctgcggcac GCTgaacgaa
1501 ccgccccCCG TGCCCGTCAG CGCAACCACC ATCGTCAAAC AGTCCAAAAAT

```

```

1551 CAAAAAAGGT GGCAAAACCG GCGTGTCAT CGACGGCGAA GACGGCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTC GTCCACCGCA AAACCTGCCC
1701 CTCTTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTCACG CTCGAAGTCA AACAAgtCAA CGacCTCCCG
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAA GGCATATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDEL DLLPD AVAATLLADI GRYVPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVCLI KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFLDILRTEL KKYNIHFEVA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGFDDY
251 IANPKGNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 GKGD SAYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLT
351 HGKVL SLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIROQNA DT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
501 PPPVPVSATT IVKQSKIKKG GKTGVLIDGE DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTA VQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDKV GVL SVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAAACTCA AGAAATACAA TGTCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTTACA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGGAAG ACAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCCGTG TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAACTC TTGGACTGGC GCGAAAACAT GCGGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAAA ACCGAGCTTT TCAACGACAC
501 GATTATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCGCT
651 CGAAAACGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCGCGGTC CAACTCGACA AACAGCTTGC CAAACTCAG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT AAAAAAGCC AGAAGACCTC
901 TACACCGCCG TCGGACAAGG CGAAATTTCC AACCGCGCCA TCCAAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCGCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTTCAg
1151 TGCACCGCAA AwyyTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCCC
1201 GAWAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTTGCGCG
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGGA AGCCAGCATG AGGTTACGCG TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCCGC GCGTCCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCGG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)


```

1... VKLKKYNVHF EVAGRPKHIY SIYKKMVKKK LSF DGLFDIR AVRILVDTVP
51 ECYTTLGIVH SLWQIPGGEF DDYIANPKGN GYKSLHTVIV GPEDKGVEVQ
101 IRTFDMHQFN EFGVAAHWRY KEGGKGSAY EQKIAWLRQL LDWRENMAES
151 GKEDLAAAFK TELFNDTIYV LTPHGKVLSL PTGATPIDFA YALHSSIGDR
201 CRGAKVEGQI VPLSTPLENG QRVEIITAKE GHPSVNWLYE GWVKSNAIG
251 KIRAYIRQN ADTVREEGRV QLDKQLAKLT PKPNLQELAE NLGYKKPEDL
301 YTAVGQGEIS NRAIQACGT LNEPPVPVVS ETTIVKQSKI KKGKNGVLI
351 DGEDGLMTTL AKCKPAPPD DIIGFVTRER GISVHRKXXX SFQHLAEHAP
401 XKVLDASWAA LQEGQVFAVD IEIRAQDRSG LLRDVSDALA RHKLNVTAVQ
451 TQSRDLEASM RFTLEVQVN DLPRVLASLG DVKGVLSVTR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/g117

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
g117	EKYREIALLLDEKRTERLEYIENFLDILRTELKKYNHFEVAGRPKHIYSIYKKMVKKKL					
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTLGI	VHSLWQIPGGEFDDYIANPKGN	GYKSLHTVIVG		
g117		SFDGLFDIRAVRILVDTVPECYTTLGI	VHSLWQIPGGEFDDYIANPKGN	GYKSLHTVIVG		
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFNEFGVAAHWRY	KEGGKGSAYEQKIAWLRQLLDWRENMAESG			
g117		PEDKGVEVQIRTFDMHQFNEFGVAAHWRY	KEGGKGSAYEQKIAWLRQLLDWRENMAESG			
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLT	PHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEGQIV	
g117		KEDLAAAFKTELFNDTIYVLT	PHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEGQIV	
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQRVEIITAKEGHPSVNWLYE	GWVKSNAIGKIRAYIRQNADTVREEGRVQ			
g117		PLSTPLENGQRVEIITAKEGHPSVNWLYE	GWVKSNAIGKIRAYIRQNADTVREEGRVQ			
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAEN	LGKYPEDLYTAVGQGEIS	NRAIQACGT	LNEPPVPVSE	
g117		LDKQLAKLTPKPNLQELAEN	LGKYPEDLYTAVGQGEIS	NRAIQACGT	LNEPPVPVSA	
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKI	KKGKNGVLIDGEDGLMTTLAKCKPAPPDDI	IGFVTRERGISVHRKXXXS		
g117		TTIVKQSKI	KKGKNGVLIDGEDGLMTTLAKCKPAPPDDI	IGFVTRERGISVHRKTCPS		
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDASWAA	LQEGQVFAVDIEIRAQDRSG	LLRDVSDALARHKL	NVTAVQT	
	400	410	420	430	440	450

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g117	FRHLAEHAPEKVLDSWAALQEGQVFAVDIEIRAQDRSGLLRDVSALARHKLNVTAQT
	570 580 590 600 610 620
m117.pep	QSRDLEASMRFTLEVQVNDLPRVLASLGDVKGVLVSVTRLX
g117	QSRDLEASMRFTLEVQVNDLPRVLAGLGDVKGVLVSVTRLX
	630 640 650 660

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 415>:

a117.seq

```

1  ATGGTTCATG  AACTCGACCT  GCTCCCCGAT  GCCGTCGCCG  CCACCCTGCT
51  TGCCGACATC  GGACGCTACG  TCCCCGACTG  GAACCTATTG  GTTTCGGAAC
101 GCTGCAACAG  TACCGTCGCC  GAGCTGGTCA  AAGGTGTGGA  CGAAGTGCAG
151 AAACTCACCC  ACTTCGCCCG  GGTGGACAGC  CTCGCCACGC  CGGAAGAACC
201 CGCCCGAGCAG  GCAGAACTA  TGCGGAAAAT  GCTGCTGGCG  ATGGTTACCG
251 ACATCCGCGT  CGTGTTAATC  AAATGGCGA  TGCGTACGCG  CACCCTGCAA
301 TTTTAAAGCA  ACGCCCCGGA  CAGCCCCGAA  AAACGCGCCG  TCGCCAAAGA
351 AACCCTCGAC  ATCTTCGCCC  CGCTCGCCAA  CCGTTTGGGC  GTGTGGCAGC
401 TCAAATGGCA  GCTCGAAGAT  TTGGGCTTCC  GCCATCAAGA  ACCCGAAAAA
451 TACCGCGAAA  TCGCCCTGCT  TTTGGACGAA  AAACGCACCG  AACGCCTCGA
501 ATACATCGAA  AACTTCCTTA  ATATCCTGCG  TACGGAATC  AAAAAATACA
551 ATATCCACTT  TGAAGTCGCC  GGCCGTCGCA  AACACATCTA  CTCCATTTAC
601 AAAAAATGG  TGAAGAAAAA  ACTCAGCTTC  GACGGGTGT  TCGACATCCG
651 CGCCGTGCGG  ATTCTGGTTG  ATACCGTCCC  CGAGTGTTAC  ACCACACTGG
701 GCATTGTCCA  CAGCCTCTGG  CAGCCCATTC  CCGGCGAGTT  CGACGACTAC
751 ATCGCCAACC  CGAAAGGCAA  CGGCTATAAA  AGTTTGCACA  CCGTCATCGT
801 CGGCCCGGAA  GACAAAGGCG  TGAAGTGCA  AATCCGCACC  TTCGATATGC
851 ACCAATTCAA  CGAATTCGGT  GTCGCCGCGC  ACTGGCGTTA  CAAAGAGGGC
901 GGCAAAGCG  ATTCCGCCTA  CGAACAAAAA  ATCGCCTGGT  TACGCCAACT
951 TTTGGACTGG  CGCGAAAACA  TGGCGGAAAG  CGGCAAGGAA  GACCTCGCCG
1001 CCGCCTTCAA  AACCAGGCTT  TTCAACGACA  CGATTTATGT  TTTGACCCCG
1051 CACGGCAAAG  TCCTCTCCCT  GCCACAGGC  GCGACCCCA  TCGACTTCGC
1101 CTACGCCCTG  CACAGCAGCA  TCGGCGACCG  TTGCCGCGGT  GCGAAAGTCG
1151 AAGGGCAGAT  TGTGCCGTG  TCCACCCCGC  TCGAAAACGG  ACAGCGTGTC
1201 GAAATCATTA  CCGCCAAAGA  AGGCATCCT  TCCGTCAACT  GGCTTTACGA
1251 AGGCTGGGTC  AAATCCAACA  AGGCAATCGG  CAAAATCCGC  GCCTACATCC
1301 GCCAGCAAAA  CGCCGACACC  GTGCGCGAAG  AAGGCCGCGT  CCAACTCGAC
1351 AAACAGCTTG  CCAAATCAC  GCCCAAACCC  AACCTGCAAG  AGCTTGCCGA
1401 AAATCTCGGC  TACAAAAGC  CAGAAGACCT  CTACACCGCC  GTCGGAACAG
1451 GCGAAATTC  CAACCGCGCC  ATCCAAAAG  CCTGCGGCAC  GCTGAACGAA
1501 CCGCCGCCCG  TACCCGTCAG  CGAAACCACC  ATCGTCAAAC  AGTCCAAAAT
1551 CAAAAAGGC  GGCAAAAACG  GCGTGCTCAT  CGACGGCGAA  GACGGTCTGA
1601 TGACCACGCT  TGCCAAATGC  TGCAAACCCG  CGCCGCCCGA  CGACATTGTC
1651 GGCTTCGTTA  CCCGCGATCG  CGGCATTTTC  GTACACCGCA  AAACCTGCCC
1701 CTCTTTCCGA  CACCTCGCCG  AACACGCGCC  CGAAAAGTA  CTGGACGCAA
1751 GTTGGGCGGC  GTTGCAAGAA  GGACAAGTGT  TCGCCGTCGA  TATCGAAATC
1801 CGCGCCCAAG  ACCGCTCCGG  GCTTTTGCGC  GACGTATCCG  ACGCGCTCGC
1851 CCGCCACAAA  CTCAACGTTA  CCGCCGTGCA  AACCAGTCC  CGCGACTTGG
1901 AAGCCAGCAT  GAGGTTACG  CTCGAAGTCA  AACAAGTTAC  CGACCTCCCA
1951 CGCGTCCTCG  CCAGCCTCGG  CGACGTCAAA  GGCGTATTGA  GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 416; ORF 117.a>:

a117.pep

```

1  MVHELDLLPD  AVAATLLADI  GRYVPDWNLL  VSERCNSTVA  ELVKGVDEVQ
51  KLTHFARVDS  LATPEERAQQ  AETMRKMLLA  MVTDIRVLI  KLAMRTRTLQ
101  FLSNAPDSPE  KRAVAKETLD  IFAPLANRLG  VWQLKWQLED  LGFRHQEPEK
151  YREIALLLDE  KRTERLEYIE  NFLNILRTEL  KKYNIHFEVA  GRPKHIYSIY
201  KKMVKKKLSF  DGLFDIRAVR  ILVDTVPECY  TTLGIVHSLW  QPIPGFEDDY
251  IANPKGNGYK  SLHTVIVGPE  DKGVEVQIRT  FDMHQFNEFG  VAAHWRYKEG
301  GKGDSEYEQK  IAWLRQLLDW  RENMAESGKE  DLAAAFKTEL  FNDTIYVLTP
351  HGKVLSLPTG  ATPIDFAYAL  HSSIGDRCRG  AKVEGQIVPL  STPLENGQRV

```

333

401 EIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQQNADT VREEGRVQLD
 451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
 501 PPPVPVSETT IVKQSKIKKG GKNGVLIDGE DGLMTTLAKC CKPAPPDDIV
 551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
 601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVTDLP
 651 RVLASLGDVK GVLSVTRL*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
a117	EKYREIALLLDEKRTERLEYIENFLNIRTELKKYNHFEVAGRPKHIYSIYKKMVKKKL					
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGFDDYIANPKGNGYKSLHTVIVG				
a117	SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGFDDYIANPKGNGYKSLHTVIVG					
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGD SAYEQKIAWLRLDWRNMAESG				
a117	PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGD SAYEQKIAWLRLDWRNMAESG					
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV				
a117	KEDLAAAFKTELFNDTIYVLTTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV					
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQ RVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ				
a117	PLSTPLENGQ RVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ					
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLG YKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPVPVSE				
a117	LDKQLAKLTPKPNLQELAENLG YKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPVPVSE					
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKIKKGGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKXXXS				
a117	TTIVKQSKIKKGGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRDRGISVHRKTCPS					
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDA SWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT				
a117	FRHLAEHAPEKVLDA SWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT					
	570	580	590	600	610	620
m117.pep		460	470	480	490	
		QSRDLEASMRFTLEVKQVNDLPRVLASLGDVKGVLSVTRLX				
a117	QSRDLEASMRFTLEVKQVTDLPRVLASLGDVKGVLSVTRLX					
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAAAGCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCCTGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCAGCAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCGGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCGGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GGAAAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCCGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCGCC ATCAAGAACC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAAC TTCCTCGATA TCCTGCGTAC GGAACATAAA
751 AAATACAATA TCCACTTTGA AGTCGCGCGC CGTCCGAAAC ACATCTACTC
801 CATTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCGTGTTCG
851 ACATCCGCGC CGTGCAGGAT CTGGTCGATA CCGTCCCCGA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGCacc AATTcAaCga ATTcGGTgTC GCCGCCCACT GGCGTTACAA
1101 AGAAGGCGGC AAAGGCGATT CCGCTACGA ACAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAATATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGCGG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGGCGAAGAC
1801 GGCTTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCGACGA
1851 TATTGCCGCG TTCGTTACCC GCGAGCGCGG CATTTCGCTC CACCGCAAAA
1901 CCTGCCCTC TTTCCGACAC CTTGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGG CAAGTGTTCT CCGTCGATAT
2001 CGAAATCCGC GCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAATC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGC GTCCCTCGCG GCCTCGGCGA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1   MTAISPIQDT QSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKYS LHTVIVGPPE KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRRCGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPS VNWLYEGWVK SGKAIGKIRA
501 YIRQQNADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRETL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

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```

51  ATTGCGCGAA  TGGTTCGACA  GCTACTGCGC  CGCTCTGCCG  GACAACGATA
101 AAAACCTCAT  CGGTACCGCA  TGGTTGCTGG  CGCAGGAACA  TTACCCCGCC
151 GATGCCGCCA  CGCCGTATGG  CGAGCCGCTG  CCCGACCACT  TCCTCGGCGC
201 GCGCGAAATG  GTTCATGAAC  TCGACCTGCT  CCCCAGTGCC  GTCGCCGCCA
251 CCCTGCTTGC  CGACATCGGA  CGCTACGTCC  CCGACTGGAA  CCTATTGGTT
301 TCCGAACGCT  GCAACAGTAC  CGTCGCCGAG  CTGGTCAAAG  GTGTGGACGA
351 AGTGCAGAAA  CTCACCCACT  TCGCCCGGGT  GGACAGCCTC  GCCACGCCGG
401 AAGAACGCGC  CCAGCAGGCA  GAAACTATGC  GGAAAATGCT  GCTGGCGATG
451 GTTACCAGCA  TCCGCGTCGT  GTTAATCAAA  CTGGCGATGC  GTACGCGCAC
501 CCTGCAATTT  TTAAGCAACG  CCCCCGACAG  CCCCCAAAAA  CGCGCCGTCG
551 CCAAAGAAAC  CCTCGACATC  TTCGCCCCGC  TCGCCAACCG  TTTGGGCGTG
601 TGGCAGCTCA  AATGGCAGCT  CGAAGATTG  GGCTTCCGCC  ATCAAAAGCC
651 CGAAAAATAC  CGCGAAATCG  CGCTGCTTTT  GGACGAAAAA  CGCACCGAAC
701 GCCTCGAATA  CATCGAAAAA  TTCTCAACA  TCCTGCGCGG  TGAACCAAG
751 AAATACAATG  TCCATTTTCA  AGTCGCCGGC  CGCCCGAAAC  ACATCTACTC
801 CATTTCACAA  AAAATGGTGA  AGAAAAAAT  CAGCTTCGAC  GGCTCTTTG
851 ACATCCGCGC  CGTGCGAATT  CTGGTTGATA  CCGTCCCGCA  GTGTTACACC
901 ACGCTGGGTA  TCGTCCACAG  CCTCTGGCAG  CCCATTCCCG  GCGAGTTTCA
951 CGACTACATC  GCCAATCCCA  AAGGCAACGG  CTATAAAAGT  TTGCACACCG
1001 TCATCGTCGG  CCCGGAAGAC  AAAGGCGTGG  AAGTACAAAT  CCGCACCTTC
1051 GATATGCACC  AATTCAACGA  ATTCGGGTGC  GCCGCCCACT  GGCGTTACAA
1101 AGAGGGCGGC  AAGGGCGATT  CCGCTACGA  ACAGAAAATC  GCCTGGTTGC
1151 GCCAACTCTT  GGACTGGCGC  GAAAACATGG  CGGAAAGCGG  CAAGGAAGAC
1201 CTCGCCGCGC  CCTTCAAAAC  CGAGCTTTTC  AACGACACGA  TTTATGTTTT
1251 GACCCCGCAC  GGCAAAGTCC  TCTCCCTGCC  CACGGGCGCG  ACCCCCATCG
1301 ACTTCGCCTA  CGCCTGCAC  AGCAGCATCG  GCGACCGTTG  CCGCGGTGCG
1351 AAAGTCGAAG  GGCAGATTGT  GCCGTGTCC  ACCCCGCTCG  AAAACGGACA
1401 GCGCGTCGAA  ATCATTACCG  CCAAAGAAGG  GCATCCTTCC  GTCAACTGGC
1451 TTTACGAAGG  CTGGGTCAAA  TCCAACAAGG  CAATCGGCAA  AATCCGCGCC
1501 TACATCCGCC  AGCAAAACGC  CGACCCGTG  CGCGAAGAAG  GCCCGTCCA
1551 ACTCGACAAA  CAGCTTGCCA  AACTCACGCC  CAAACCCAAC  CTGCAAGAGC
1601 TTGCCGAAAA  TCTCGGCTAC  AAAAAGCCAG  AAGACCTCTA  CACCGCGTTC
1651 GGACAAGGCG  AAATTTCCAA  CCGCGCCATC  CAAAAAGCCT  CCGGCACGCT
1701 GAACGAACCG  CCGCCCGTAC  CCGTCAGCGA  AACCACCATC  GTCAAAACAGT
1751 CCAAAATCAA  AAAAGGCGGC  AAAAACGGCG  TGCTCATCGA  CGGCGAAGAC
1801 GGTCTGATGA  CCACGCTTGC  CAAATGCTGC  AAACCCGCGC  CGCCCCGACG
1851 TATTATCGGC  TTCGTTACCC  GCGAGCGCGG  CATTTACAGT  CACCGCAAAA
1901 CCTGCCCGTC  TTTCCAACAC  CTCGCCGAAC  ACGCGCCCGA  AAAAGTGCTG
1951 GAGCGAAGCT  GGGCGGCATT  GCAGGAAGGA  CAAGTATTCG  CCGTCGATAT
2001 CGAAATCCGC  GCCCAAGACC  GTCGCGGCT  TTTGCGCGAC  GTATCCGACG
2051 CGCTCGCCCG  CCACAAACTC  AACGTTACCG  CCGTGCAAAAC  CCAGTCCCGC
2101 GACTTGGAAG  CCAGCATGAG  GTTCACGCTC  GAAGTCAAAAC  AAGTCAACGA
2151 CCTCCGCGCG  GTCCTCGCCA  GCCTCGGCGA  CGTCAAAGGC  GTATTGAGCG
2201 TTACCCGGCT  TTAA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT  QSATLQELRE  WFDSYCAALP  DNDKNLIGTA  WLLAQEHYPA
51  DAATPYGEPL  PDHFLGAAQM  VHELDLLPDA  VAATLLADIG  RYVPDWNLLV
101 SERCNSTVAE  LVKGVDEVOK  LTHFARVDSL  ATPEERAQQA  ETMRKMLLAM
151 VTDIRVVLIK  LAMRTRTLQF  LSNAPDSPEK  RAVAKETLDI  FAPLANRLGV
201 WQLKWQLEDL  GFRHQKPEKY  REIALLLDEK  RTERLEYIEN  FLNILRGELK
251 KYNVHFEVAG  RPKHIYSIYK  KMVKKKLSFD  GLFDIRAVRI  LVDTVPECYT
301 TLGIVHSLWQ  PIPGEFDDYI  ANPKNGNGYKS  LHTVIVGPED  KGVEVQIRTF
351 DMHQFNEFGV  AAHWRYKEGG  KGDSAYEQKI  AWLRQLLDWR  ENMAESGKED
401 LAAAFKTELF  NDTIYVLTPL  GKVLSLPTGA  TPIDFAYALH  SSIGDRCRGA
451 KVEGQIVPLS  TPLENGQORVE  IITAKEGHPS  VNWLYEGWVK  SNKAIGKIRA
501 YIRQQNADTV  REEGRVQLDK  QLAKLTPKEN  LQELAENLGY  KKPEDLYTAV
551 GGGEISNRAI  QKACGTLNEP  PPVPVSETTI  VKQSKIKKGG  KNGVLIDGED
601 GLMTTLAKCC  KPAPDDIIG  FVTRERGISV  HRKTCPSFOH  LAEHAPEKVL
651 DASWAALQEG  QVFAVDIEIR  AQDRSGLLRD  VSDALARHKL  NVTAVQTQSR
701 DLEASMRFTL  EVKQVNDLPR  VLASLGDVKG  VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFSYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFSYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m117-1.pep PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
g117-1      PDHFLGAAQMVDELDDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
              70      80      90      100     110     120

              130     140     150     160     170     180
m117-1.pep LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK
g117-1      LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK
              130     140     150     160     170     180

              190     200     210     220     230     240
m117-1.pep RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN
g117-1      RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQEPEKYREIALLLDEKRTERLEYIEN
              190     200     210     220     230     240

              250     260     270     280     290     300
m117-1.pep FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
g117-1      FLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
              250     260     270     280     290     300

              310     320     330     340     350     360
m117-1.pep TLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTDFDMHQFNEFGV
g117-1      TLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVGPEEKGVEVQIRTDFDMHQFNEFGV
              310     320     330     340     350     360

              370     380     390     400     410     420
m117-1.pep AAHWRYKEGGKGSAYEQKIAWLRLQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
g117-1      AAHWRYKEGGKGSAYEQKIAWLRLQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
              370     380     390     400     410     420

              430     440     450     460     470     480
m117-1.pep GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQRVETITAKEGHPS
g117-1      GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQRVETITAKEGHPS
              430     440     450     460     470     480

              490     500     510     520     530     540
m117-1.pep VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
g117-1      VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
              490     500     510     520     530     540

              550     560     570     580     590     600
m117-1.pep KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED
g117-1      KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSATTIVKQSKIKKGGKTGVLIDGED
              550     560     570     580     590     600

              610     620     630     640     650     660
m117-1.pep GLMTTLAKCCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG
g117-1      GLMTTLAKCCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG
              610     620     630     640     650     660

              670     680     690     700     710     720
m117-1.pep QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEVQVNDLPR
g117-1      QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEVQVNDLPR
              670     680     690     700     710     720

              730
m117-1.pep VLASLGDKVGVLSVTRLX
g117-1      VLAGLGDKVGVLSVTRLX
              730

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m117-1/RelA

sp|P55133|RELA_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744
Score = 536 bits (1366), Expect = e-151
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRYVPDWNLLVSERCNSTVAELVKGVDVQKLTHFARVDSL 130
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S
Sbjct: 68 LSMADTLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVQMC AIS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEKRAVAKETLDI 190
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I
Sbjct: 122 AEETAQAAQVDNIRRMLLSMVDDFRCVVIKLAERICNLREVKDQDPDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWQLKWOLEDLGRHQKPEKYREIALLDEKRTERLEYIENFLNIRGELK 250
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDQTYKQIAKQLSERRIDREDYITHFVDDLS DAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKKMVKKKLSFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQ 310
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++
Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGVAHHWRYKEG- 369
+P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHHW+YKEG
Sbjct: 301 HLPKEFDDYVANPKNGYQSIHTVVLGPEGKTIEIQIRTKMHHESELGVAHHWRYKEGT 360

Query: 370 --GKGDSAYEQIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPHGKVL SLP 427
G SAY++KI WLR+LL W+E M++SG ++ ++++F+D +Y TP G V+ LP
Sbjct: 361 ASGGAQSAYDEKINWLRKLLAQEEMSDSG--EMLDELRSQVFFDRVYAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRRCGAKVEGQIVPLSTPLENGQRVEIITAKEGHPNVNWL YE- 486
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAIGKIRAYIRQQNADTVREGRVQLDKQLAKL--TPKPNLQELAE NLGYKKP 543
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDKNIIAGKEILEAEVLKIHATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGT LNEPPVPVSETTIVKQSKI-----KKGKNGV 594
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V
Sbjct: 539 EELYAGTGSGLRINQVINHINALVNKPTAEEDQQLLEKLSEASNQATSHKKPORDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPKVL DNASW 654
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W
Sbjct: 599 VVEGVNDLNMTHLARCCQPIPGDDIQGFVTQGRGISVHRMDCEQLEELRHHPERIIDTVW 658

Query: 655 AALQEGQVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQ--SRDLEASMRFTLEV 712
G + + + + A +R+GLL++++ L K+ V ++++ + + M F LE+
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLLKELNTLMNEKVKVAGMKSRVDYKKQMSIMDFE LEL 717

Query: 713 KQVNDLPRVLASLGDKGVLSVTRL 737
+ L RVL + VK V RL
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

all17-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACAACGATA
101  AAAAATTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GCGCAAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCCGCCA
251  CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351  AGTGCAGAAA CTCACCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401  AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAATATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTAATCAAA CTGGCGATGC GTACGCGCAC
501  CCTGCAATTT TTAAGCAACG CCCCCGACAG CCCCCGAAAA CGCGCCGTCG
551  CCAAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG TTGGGCGGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAACC
651  CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701  GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAAC TCAA
751  AAATACAATA TCCACTTTGA AGTCGCCGGC CGTCCGAAAC ACATCTACTC
801  CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGGTTGTTCC

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851 ACATCCGCGC CGTGCGGATT CTGGTTGATA CCGTCCCCGA GTGTTACACC
901 ACACCTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCC GCGAGTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGTGTC GCCGCGCACT GGCGTTACAA
1101 AGAGGGCGGC AAAGGCGATT CCGCCTACGA AAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGA CTGGCGC GAAAACATGG CCGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGTGTCAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGCTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGGCGCG AAAAACGCGG TGCTCATCGA CCGCGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 CATTGTGCGG TTCGTTACCC GCGATCGCGG CATTTCGTA CACCGCAAAA
1901 CCTGCCCTC TTTCCGACAC CTCGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GAGCGAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTTC GCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGAAG CCAGCATGAG GTTACGCTC GAAGTCAAAC AAGTTACCGA
2151 CCTCCACGC GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTAGCG
2201 TTACCCGCT TAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

a117-1.pep

```

1 MTAISPIQDT QSATLQELRE WFD SYCTALP NNDKKLVLA RSLAEAHYPA
51 DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIHFVAVG RPKHIYSIYK KMKVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSGIDRCRGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPS VNWLIEGWVK SNKAIGKIRA
501 YIRQQNADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKI KKG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

```

a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
a117-1	MTAISPIQDTQSATLQELREWFD SYCTALPNNDKKLVLAARS LAE AHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m117-1.pep	PDHFLGAAQM VHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQM VHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK					
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQEPEKYREIALLLDEKRTERLEYIEN					
	190	200	210	220	230	240

m117-1.pep	250	260	270	280	290	300
	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
a117-1	FLNILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
	250	260	270	280	290	300
m117-1.pep	310	320	330	340	350	360
	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
a117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
	310	320	330	340	350	360
m117-1.pep	370	380	390	400	410	420
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH					
a117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH					
	370	380	390	400	410	420
m117-1.pep	430	440	450	460	470	480
	GKVLSTPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	GKVLSTPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
	430	440	450	460	470	480
m117-1.pep	490	500	510	520	530	540
	VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
a117-1	VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
	490	500	510	520	530	540
m117-1.pep	550	560	570	580	590	600
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
a117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
	550	560	570	580	590	600
m117-1.pep	610	620	630	640	650	660
	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAHAPEKVLDAASWAALQEG					
a117-1	GLMTTLAKCKPAPPDDIIGFVTRDRGISVHRKTCPSFRHLAHAPEKVLDAASWAALQEG					
	610	620	630	640	650	660
m117-1.pep	670	680	690	700	710	720
	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEV KQVNDLPR					
a117-1	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEV KQVNDLPR					
	670	680	690	700	710	720
m117-1.pep	730					
	VLASLGDVKGVL SVTRLX					
a117-1	VLASLGDVKGVL SVTRLX					
	730					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1   ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1   MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRRK
51  YPYPM DIPRD IVIGIGTIID FLMV PNWELF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*

```

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
  1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
 51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101  ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151  TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTTCATTG GAATCGGTAC
201  CATTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTTT GAAATTAAG
251  CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301  TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351  GCGATTTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
  1  MCEFKDIIRN VPFEGYDEN SFIGKYYDDG VWDDEEYWKL ENDLIEVRKK
 51  YPYPM DIPRY VVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101  FTTMLRYIFT EKDIVNVRFD YYNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

      10      20      30      40      50      60
m118.pep  MCEFKDIIRNVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||
g118      MCEFKDFRRNIPCFEEYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60

      70      80      90     100     110     120
m118.pep  VVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g118      IVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          70      80      90     100     110     120

m118.pep  YYNKKX
          |||||
g118      YYNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
  1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
 51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101  ATGAAGAATA TTGGAATTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151  TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201  CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTTT GAAATTAAG
251  CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301  TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351  GCGATTTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
  1  MCEFKDFRRN IPCFEEYDEN SFIGKYYDDG VWDDEEYWKL ENDLIEVRKK
 51  YPYPM DIPRD IVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101  FTTMLRYIFT EKDIVNVRFD YYNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep      10      20      30      40      50      60
MCEFKDIIRNVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
|||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||
a118          MCEFKDFRRNIPCFEEYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
              10      20      30      40      50      60
```

		70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLFEIKASPLPDSVGIERHERYERFTTMLRYIFTEKDIVNVRFD						
a118	: : : : : : : : : : :						
	IVIGIGTIIDFLMVPNWELFEIKASPLPDSVGIERHERYERFTTMLRYIFTEKDIVNVRFD						
		70	80	90	100	110	120
m118.pep	YYNKXX						
a118	YYNKXX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

g120.seq

1	ATGATGAAGA	CTTTTAAAAA	TATATTTTCC	GCCGCCATT	TGTCCGCCGC
51	CCTGCCGTGC	GCGTATCGCG	CAAGGCTACC	CCAATCCGCG	GTGCTGCAC
101	ATTCCGGCAG	CTACGGCATT	CCCGCCACGA	TGACATTGTA	ACCGACGCGC
151	AATGCTTACA	AAATCGTTTC	GACGATTAAG	GTGCCGTGAT	ACAATATCCG
201	TTTCGAATCC	GGCGGTACGG	TTGTCGGCAA	TACCTGCAC	CCTGCCTACT
251	ATAAAGACAT	ACGCAGGGGC	AAACTGTATG	CGGAAGCCAA	ATTCCGCGAC
301	GGCAGCGTAA	CCTACGGCAA	AGCGGGCGAG	AGCAAAACCG	AGCAAAGCCC
351	CAAGGCTATG	GATTTGTCTA	CGCTTGCTGT	GCAGTTGGCG	GCAATATGAC
401	CGAAACTCCC	CCCGGGTCTG	AAATCACCAC	ACGGCAAAAA	ACTTTATTCC
451	GTCGGCGGCC	TGAATAAGGC	GGGTACGGGA	AAATACAGCA	Taggcggcgt
501	gGAAACCGAA	GTCGTCAAAT	ATCGGGTGCG	GCGCGGCCAC	GATACGGTAA
551	CGTATTCTT	CGCACCGTCC	CTGAACAATA	TTCCGGCACA	AATCGGCTAT
601	ACCGACgaCG	GCAAAACCTA	TACGCTGAAG	CTCAAATCGG	TGCAGATCAA
651	CGGACAGGCC	GCCAAACCGT	AA		

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

```
g120.pep
1  MMKTFKNIFS  AAILSAAALPC  AYAARLPQSA  VLHYSGSYGI  PATMTFERSG
51 NAYKIVSTIK  VPLYNRFES  GGTVVGNTLH  PAYYKDIRRG  KLYAEAKFAD
101 GSVTYGKAGE  SKTEQSPKAM  DLFTLAWQLA  ANDAKLPPGL  KITNGKKLYS
151 VGGLNKAGTG  KYSIGGVETE  VVKYRVRRGD  DTVTYFFAPS  LNNIPAQIGY
201 TDDGKTYTLK  LKSVQINGQA  AKP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

```
m120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCG GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGGA ACGCAGCGCG
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTGAGTCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAACGTGTAT CGGAAGCcaa ATTCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCTG CGAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGCGTG AAAATACACA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG
```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

m120.pep	1	MMKTFKNIFS	AAILSAAALPC	AYAAGLPQSA	VLXYSGSYGI	PATMTFERSG
	51	NAYKIVSTIK	VPLYNIRFES	GGTVVGNTLH	PTYYRDIRRG	KLYAEAKFAD
	101	GSVTYKGAGE	SKTESQSPKAM	DLFTLAWQLA	ANDAKLPPGL	KITNGKKLYS
	151	VGGLNKAGTG	KYSIGGVETE	VVKYRVRRGD	DAVMYFFAPS	LNNIPAQIGY
	201	TDDGKTYTLK	LKSQVINGOA	AKP		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
g120	MMKTFKNIFSAAILSAALPCAYAARLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSV TYGKAGESKTEQSPKAM					
g120	VPLYNIRFESGGTVVGNTLHPAYYKDIRRGKLYAEAKFADGSV TYGKAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRGD					
g120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA AKP					
	:					
g120	DTVTYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA KPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

1	ATGATGAAGA	CTTTTAAAAA	TATATTTTCC	GCCGCCATTT	TGTCCGCCGC
51	CCTGCCGTGC	GCGTATGCGG	CAGGGCTGCC	CCAATCCGCC	GTGCTGCACT
101	ATTCCGGCAG	CTACGGCATT	CCCGCCACGA	TGACATTTGA	ACGCAGCGGC
151	AATGCTTACA	AAATCGTTTC	GACGATTAAA	GTGCCGCTAT	ACAATATCCG
201	TTTCGAGTCC	GGCGGTACGG	TTGTCCGCAA	TACCCTGCAC	CCTACCTACT
251	ATAGAGACAT	ACGCAGGGGC	AAACTGTATG	CGGAAGCCAA	ATTCCGCCGAC
301	GGCAGCGTAA	CCTACGGCAA	AGCGGGCGAG	AGCAAAACCG	AGCAAAGCCC
351	CAAGGCTATG	GATTTGTTCA	CGCTTGCTG	GCAGTTGGCG	GCAAATGACG
401	CGAAACTCCC	CCCGGGGCTG	AAAATCACCA	ACGGCAAAAA	ACTTTATTCC
451	GTCGGCGGTT	TGAATAAGGC	GGGTACAGGA	AAATACAGCA	TAGGCGGCGT
501	GGAAACCGAA	GTCGTCAAAAT	ATCGGGTGCG	GCGCGGCGAC	GATGCGGTAA
551	TGTATTTCTT	CGCACCGTCC	CTGAACAATA	TTCCGGCACA	AATCGGCTAT
601	ACCGACGACG	GCAAAACCTA	TACGCTGAAA	CTCAAATCGG	TGCAGATCAA
651	CGGCCAGGCA	GCCAAACCGT	AA		

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

1	MMKTFKNIFS	AAILSAALPC	AYAAGLPQSA	VLHYSYGI	PATMTFERSG
51	NAYKIVSTIK	VPLYNIRFES	GGTVVGNTLH	PTYRDIRRG	KLYAEAKFAD
101	GSV TYGKAGE	SKTEQSPKAM	DLFTLAWQLA	ANDAKLPPGL	KITNGKKLYS
151	VGGLNKAGTG	KYSIGGVETE	VVKYRVRRGD	DAVMYFFAPS	LNNIPAQIGY
201	TDDGKTYTLK	LKSVQINGQA	AKP*		

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
a120	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					

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	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
a120	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRRGD					
a120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
a120	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAACAC  AGCTTTACAT  CGGCATTATG  TCGGGAACCA  GTATGGACGG
51  GCGGATGCC  GTGCTGGTAC  GGATGGACGG  CGGCAAATGG  CTGGGCGCGG
101 AAGGGCACGC  CTTTACCCCC  TACCGTGACC  GGTGCGCCG  CAAATTGCTG
151 GATTTCAGG  ACACAGGCAC  AGACGAACTG  CACCGCAGCA  GGATGTTGTC
201 GCAAGAACTC  AGCCGCCTGT  ACGCGCAAAC  CGCCGCCGAA  CTGCTGTGCA
251 GTCAAAACCT  CGCTCCGTGC  GACATTACCG  CCTCGGCTG  CCACGGGCAA
301 ACCGTCCGAC  ACGCGCCGGA  ACACGGTtac  AGCATACAGC  TTGCCGATTT
351 GCCGCTGCTG  GCGGAACTGa  cgcggatttt  TACCGTCggc  gacttcCGCA
401 GCCGCGACCT  TGCTGCCGGC  GGacaAGGTG  CGCCGCTCGT  CCCCgcCTTT
451 CACGAAGCCC  TGTTCGCGA  TGACAGGGAA  ACACGCGTGG  TACTGAACAT
501 CGGCGGGATT  GCCAACATCA  GCGTACTCCC  CCCCggCGCA  CCCGcCTTCG
551 GCTTCGACAC  AGGGCCGGGC  AATATGCTGA  TGGAcgcgtg  gacgcaggca
601 cactGGcagc  TGCCTTACGA  CAAAAacggt  gcAAAGgcgg  cacAAGGCaa
651 catatTGCcg  cAACTGCTCG  gcaggctGCT  CGCCcaccCG  TATTTCTCAC
701 AACCCcacc  aaAAAGCACG  GGgcGCGaac  TgtttgcccT  AAattggctc
751 gaaacctAcc  ttgacggcgg  cgaaaaccga  tacgacgtat  tgccgacgct
801 ttcccgattc  accgcgcaaa  ccgTttggga  cgccgtctca  CACGCAGCGG
851 CAGATGCCCG  TCAAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCCTGTT
901 TTAATGGCGG  ATTTGGCAGA  ATGTTTCGGC  ACACGCGTTT  CCCTGCACAG
951 CACCGCCGAA  CTGAACCTCG  ATCCTCAATG  GGTGGAGGCG  gccgCATTtg
1001 cgtggttgC  GGCGTGTGG  ATTAACCGCA  TCCCGGTAG  TCCGCACAAA
1051 GCGACCGGCG  CATCAAACC  GTGTATTCTG  GGCGCGGGAT  ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM  SGTSMDGADA  VLVRMDGGKW  LGAEGHAFTP  YPDLRRLKLL
51  DLQDTGTDEL  HRSRMLSQEL  SRLYAQTAAE  LLCSQNLAPC  DITALGCHGQ
101 TVRHAPEHGY  SIQLADLPLL  AELTRIFTVG  DFRSRDLAAG  GQGAPLVPAP
151 HEALFRDDRE  TRVVLNIGGI  ANISVLPPGA  PAFGFDTPG  NMLMDAWTQA
201 HWQLPYDKNG  AKAAQGNILP  QLLGRLLAHP  YFSQPHPKST  GRELFALNWL
251 ETYLDGGENR  YDVLRTLRF  TAQTVWDAVS  HAAADARQMY  ICGGGIRNPV
301 LMADLAECFG  TRVSLHSTAE  LNLDPQWVEA  AAFAWLAACW  INRIPGSPHK
351 ATGASKPCIL  GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GCGGATGCC  GTACTGATAC  GGATGGACGG  CGGCAAATGG  CTGGGCGCGG
101 AAGGGCACGC  CTTTACCCCC  TACCCCGGCA  GGTACGCCG  CCAATTGCTG

```

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```

151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTG
201 GCAAGAACTC AGCCGCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACCGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAA CCGTTTGCGA CGCGTCTCA CACGAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGENR YDVLRTLRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTPYPDRLRRKLLDLQDTGDEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRILSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLRF TAQTVCDAYS HAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLRF TAQTVWDAVS HAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLD	PQWVEAA	FAWLAACWINRIPGSPHKATGASKPCIL			
g121	LMADLAECFGTRVSLHSTAE	LNLD	PQWVEAA	FAWLAACWINRIPGSPHKATGASKPCIL		
	310	320	330	340	350	360
m121.pep	XAGYYYY					
g121	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAAGTG CACCGCAGCA GGATGTTGTC
201 GCAAGACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCG TATTTGCGAC
701 AACCCACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTC ACCGCGCAA CCGTTTTCGA CGCCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCGGAA CTGAACCTCG ATCCGCAATG GGTAAGGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWMAACW VNRI PGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFT	PYPGRLLRRQLDLQDTGADEL				
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFT	PYPGRLLRRQLDLQDTGADEL				
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQT	TVRHAPEHGYSIQLADLPLL				
a121	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQT	TVRHAPEHSYSVQLADLPLL				
	70	80	90	100	110	120

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	130	140	150	160	170	180
m121.pep	XX					
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICDGGIRNPV					
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFCDVASHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAXFAWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYY					
a121	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GCGGATGCC  GTACTGATAC  GGATGGACGG  CGGCAAATGG  CTGGGCGCGG
101 AAGGGCACGC  CTTTACCCCC  TACCCCGGCA  GGTACGCCG  CCAATTGCTG
151 GATTTGCAGG  ACACAGGCGC  AGACGAACTG  CACCGCAGCA  GGATTTTGTC
201 GCAAGAACTC  AGCCGCCTAT  ATGCGCAAAC  CGCCGCCGAA  CTGCTGTGCA
251 GTCAAAACCT  CGCACCGTCC  GACATTACCG  CCCTCGGCTG  CCACGGGCAA
301 ACCGTCCGAC  ACGCGCCGGA  ACACGGTTAC  AGCATACAGC  TTGCCGATTT
351 GCGCTGCTG  GCGGAACGGA  CGCGGATTTT  TACCGTCGGC  GACTTCCGCA
401 GCGCGACCT  TGCGGCCGGC  GGACAAGCGC  CGCCACTCGT  CCCCCTTTT
451 CACGAAGCCC  TGTTCGCGCA  CAACAGGGAA  ACACGCGCGG  TACTGAACAT
501 CGCGGGGATT  GCCAACATCA  GCGTACTCCC  CCCCACGCA  CCGCCTTCG
551 GCTTCGACAC  AGGGCCGGGC  AATATGCTGA  TGGACGCGTG  GACGACGGCA
601 CACTGGCAGC  TTCCTTACGA  CAAAACGGT  GCAAAGGCGG  CACAAGGCAA
651 CATATTGCCG  CAACTGCTCG  ACAGGCTGCT  CGCCACCCG  TATTTCGCAC
701 AACCCACCC  TAAAGCACG  GGGCGCAAC  TGTTCGCCCT  AAATTGGCTC
751 GAAACCTACC  TTGACGGCGG  CGAAAACCGA  TACGACGTAT  TCGGACGCT
801 TTCCCGTTTT  ACCGCGCAA  CCGTTGCGA  CGCGTCTCA  CACGACGGG
851 CAGATGCCCC  TCAAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCCTGTT
901 TTAATGGCGG  ATTTGCGAGA  ATGTTTCGGC  ACACGCGTTT  CCCTGCACAG
951 CACCGCCGAC  CTGAACCTCG  ATCCGCAATG  GGTGGAAGCC  GCCGNATTTG
1001 CGTGGTTGGC  GCGGTGTTGG  ATTAATCGCA  TTCCCGGTAG  TCCGCACAAA
1051 GCAACCGCGC  CATCAAACC  GTGTATTCTG  ANCGCGGGAT  ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM  SGTSMGDGADA  VLIRMDGGKW  LGAEGHAFTP  YPGLRRQLL
51  DLQDTGADEL  HRSRILSQEL  SRLYAQTAAE  LLCSONLAPS  DITALGCHGQ
101 TVRHAPHEGY  SIQLADLPLL  AERTRIFTVG  DFRSRDLAAG  QGGAPLVPAF
151 HEALFRDNRE  TRAVLNIGGI  ANISVLPPDA  PAFGFDTGPG  NMLMDAWTQA
201 HWQLPYDKNG  AKAQGNILP  QLLDRLLAHP  YFAQPHPKST  GRELFALNWL
251 ETYLDGGENR  YDVLRTLSRF  TAQTVCDVAVS  HAAADARQMY  ICGGGIRNPV
301 LMADLAECFG  TRVSLHSTAD  LNLDPQWVEA  AXFAWLAACW  INRIPGSPHK
351 ATGASKPCIL  XAGYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

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```

m121-1.pep  METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTYPYGRRLRRQLLDLQDTGADEL
|||||
g121        METQLYIGIMSGTSMGDADAVLRMDGGKWLGAEGHAFTYPYDRLRRKLLDLQDTGTDEL
          10      20      30      40      50      60

          70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL
|||||
g121        HRSRILSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
          70      80      90      100     110     120

          130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA
|||||
g121        AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA
          130     140     150     160     170     180

          190     200     210     220     230     240
m121-1.pep  PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
|||||
g121        PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
          190     200     210     220     230     240

          250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDAVSHAAADARQMYICGGGIRNPV
|||||
g121        GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIRNPV
          250     260     270     280     290     300

          310     320     330     340     350     360
m121-1.pep  LMADLAECFGRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
|||||
g121        LMADLAECFGRVSLHSTAEELNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
          310     320     330     340     350     360

m121-1.pep  XAGYXX
|||||
g121        GAGYXX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1  ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GCGGATGCC  GTACTGATAC  GGATGGACGG  CGGCAATGG  CTGGGCGCGG
101  AAGGGCACGC  CTTTACCCC  TACCCCGGCA  GGTACGCGG  CAAATGCTG
151  GATTGTCAGG  ACACAGGCGC  GGACGAACTG  CACCGCAGCA  GGATGTTGTC
201  GCAGAACTC  AGCCGCCTGT  ACGCGCAAAC  CGCCGCGGAA  CTGCTGTGCA
251  GTCAAAACCT  CGCGCCGTCC  GACATTACCG  CCCTCGGCTG  CCACGGGCAA
301  ACCGTCAGAC  ACGCGCCGGA  ACACAGTTAC  AGCGTACAGC  TTGCCGATTT
351  GCCGCTGCTG  GCGGAACGGA  CTCAGATTTT  TACCGTCGGC  GACTTCGCGA
401  GCCGCGACCT  TGCGGCCGGC  GGACAAGGCG  CGCCGCTCGT  CCCCCTTTT
451  CACGAAGCCC  TGTTCCGCGA  CGACAGGGAA  ACACGCGCGG  TACTGAACAT
501  CGGCGGGATT  GCCAACATCA  GCGTACTCCC  CCCCAGCGCA  CCCCCTTCG
551  GCTTCGACAC  AGGACCGGGC  AATATGCTGA  TGACGCGGTG  GATGCAGGCA
601  CACTGGCAGC  TTCCTTACGA  CAAAACGGT  GCAAAGCGCG  CACAAGGCAA
651  CATATTGCGG  CAACTGCTCG  ACAGGCTGCT  CGCCACCCG  TATTTCGCAC
701  AACCCACCC  TAAAAGCACG  GGGCGCGAAC  TGTTGCCCT  AAATTGGCTC
751  GAAACCTACC  TTGACGGCGG  CGAAAACCGA  TACGACGTAT  TGCGGACGCT
801  TTCCCGATT  ACCGCGCAAA  CCGTTTCGA  CGCCGTCTCA  CACGAGCGG
851  CAGATGCCCG  TCAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCTGTT
901  TTAATGGCGG  ATTTGGCAGA  ATGTTTCGGC  ACACGCGTTT  CCCTGCACAG
951  CACGCGCGAA  CTGAACCTCG  ATCCGCAATG  GGTAGAAGCC  GCCGCTTCG
1001  CATGGATGGC  GCGGTGTTGG  GTCAACCGCA  TTCCCGTAG  TCCGCACAAA
1051  GCAACCGCG  CATCCAAACC  GTGTATTCTG  GCGCGGGAT  ATTATTATTG
1101  A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM  SGTSMGDADA  VLIRMDGGKW  LGAEGHAFTP  YPGRRLRRKLL
51  DLQDTGADEL  HRSRILSQEL  SRLYAQTAAE  LLCSQNLAPS  DITALGCHGQ
101  TVRHAPEHSY  SVQLADLPLL  AERTQIFTVG  DFRSRDLAAG  GQGAPLVPF
151  HEALFRDDRE  TRAVLNIGGI  ANISVLPPDA  PAFGFDTGPG  NMLMDAWMQA

```

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201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121-1/a121-1 96.4% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRL	RRLQLLDLQDTGA	DEL	
a121-1	10	20	30	40	50	60
	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRL	RRLKLLDLQDTGA	DEL	
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPEHGYSI	QLADLPLL	
a121-1	70	80	90	100	110	120
	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPEHSYSV	QLADLPLL	
m121-1.pep	130	140	150	160	170	180
	AERTRIFTVGDF	RSRDLAAGGQGA	PLVPFHEALFRD	NRETRAVLNIGG	IANISVLPPDA	
a121-1	130	140	150	160	170	180
	AERTQIFTVGDF	RSRDLAAGGQGA	PLVPFHEALFRD	DRETRAVLNIGG	IANISVLPPDA	
m121-1.pep	190	200	210	220	230	240
	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRL	LAHPYFAQPHPK	ST
a121-1	190	200	210	220	230	240
	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRL	LAHPYFAQPHPK	ST
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVCDVSHAAAD	ARQMYICGGGI	RNPV
a121-1	250	260	270	280	290	300
	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVFVDAVSHAA	ADARQMYICGG	GIRNPV
m121-1.pep	310	320	330	340	350	360
	LMADLAECFG	TRVSLHSTAD	LNLDPQWVEA	AAXFAWLAAC	WINRIPGSPHK	KATGASKPCIL
a121	310	320	330	340	350	360
	LMADLAECFG	TRVSLHSTAE	LNLDPQWVEA	AAFAWMAACW	VNRIPGSPHK	KATGASKPCIL
m121-1.pep						
	XAGYYYY					
a121						
	GAGYYYY					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGGA AAAAGCGCAA GtcatCGTAC
101 TGCTGGGCCC gTccggctgc ggCAAATCCA CCTTectgcg ctgcgtaac
151 GGTTTGGAGC CGCACCagg cgGCAGCATC GTGATGGACG GTgtcgGCGA
201 ATTCggcAAA GACGTTTCCT GGCAAACCGC CCGCAAAAa gtcggtatgg
251 tctttcaaag taacgAactg Tttgcccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAACgC gaccgtgccg aagcaGAGGC
351 gCAAGCCGCG AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GGCGGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGGACG AAATCACC GC
501 CGCACTTGAC CCCGAAATGG TGC CGGAAGT CTTGGAAGTG GTTTTGG AAC
551 TCGCCCGCGA AGGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCCGAAA CCTTTTTC CGCACCAAAA AGCGAACCGC
701 CCCGCCAATT TCTGGCAGGT ATGGACTACT GA
```

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 447>:

m122.seq

This corresponds to the amino acid sequence <SEQ ID 448; ORF 122>:

m122.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng) from *N. gonorrhoeae*:

m122/g122

		10	20	30	40	50	60
m122.pep		VVMIKIRNIHKFTGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQI					
		::::: { : } : :::: { : } { : : : { { } { : : { : : { } : {					
g122		MALLSIRKLHKQYGSVTAIQSLDLDLLEKGEVIVLLGPSGCGKSTLLRCVNGLEPHQGGSI					
		10	20	30	40	50	60
		70	80	90	100	110	120
m122.pep		EFDNERPLKIDFSKKPSKHDILALRRKSXMVFQQYNLFPHKTALENVMEGPPVAVQGKPAA					
		: : : : : : : : : { : { :					
g122		VMDGVGEFGKDVSWQTA-----RQKVGVMVFQSNELFAHMTVIENIFLGPVKEQNRDRA					
		70	80	90	100	110	
		130	140	150	160	170	180
m122.pep		QAREEALKLLEKVGLGDKVDLYPYQLSGGQQORVGIARALAIQPELMLFDEPTSALDPEL					
		: : : { { : { } : : : { { : { : : { } : { : : { } { { { :					
g122		EAEAQAQAGKLLERVGLLDRKNAYPRELSGGQKQRIAIVRALCLNPEVILLDEITAAALPEM					
		120	130	140	150	160	170
		190	200	210	220	230	240
m122.pep		VQDVLDXMKELAQEGWMTMVVVTHEIKFALEVATTXVMDXGVIVEQGSPODLFDHPKHER					
		: { : : { { } : : { { } { : { } { } { { : : { } : { { } {					
g122		VREVLEVVLLELAREGMSMLIVTHEMGFARKVADRIVFMDKGGIVESSDPETFFSAPKSEI					

350

	180	190	200	210	220	230
	250					
m122.pep	TRRFLSQQSTKIX					
	: : : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```
a122.seq
1  GTTGTTCATGA  TTAAATCCG  CAATATCCAT  AAGACCTTCG  GCAAAAATAC
51  CATTTTGCGC  GGCATCAATT  TGGATGTGTG  CAAAGGGCAG  GTGGTCGTCA
101 TCCTCGGGCC  TTCCGGCTCA  GGCAAAACGA  CGTTTCTGCG  ATGCCTAAAC
151 GCGTTGGAAG  TGCCCGAAGA  CGGACAAATC  GAGTTCGACA  ACGAGCGACC
201 GCTGAAAATC  GATTTTCTTA  AAAAACCAG  CAAACACGAT  ATTTTGGCAC
251 TGCGCCGCAA  ATCAGGCATG  GTGTTTCAAC  AATACAACCT  CTTTCCGCAC
301 AAAACCGCCT  TGGAAAACGT  GATGGAAGGA  CCGGTTGCCG  TACAGGGCAA
351 GCCTGCCGCC  CAAGCGCGCG  AAGAGGCTCT  GAAACTGCTG  GAAAAAGTCG
401 GCTTGGGCGA  CAAAGTGGAT  TTGTATCCCT  ACCAGCTTTC  CGGCGGTCAG
451 CAGCAGCGCG  TCGGCATTGC  CCGAGCATTG  GCGATTACAG  CCGAGCTGAT
501 GTTGTGTTGAC  GAACCCACTT  CCGCGCTTGA  CCCCAGATTG  GTGCAAGACG
551 TGTGAACGC  CATGAAGGAA  TTGGCGCGGG  AAGGTTGGAC  GATGTCGTC
601 GTTACCCACG  AAATCAAGTT  CGCGCTGGAA  GTTGCCACGA  CCGTTGTCGT
651 GATGGACGGC  GCGGTTATCG  TAGAGCAGGG  CAGCCCGAAA  GAGTTGTTTC
701 ACCACCCCAA  ACACGAACGG  ACGCGGAGAT  TTTTAAGCCA  AATCCAATCT
751 ACCAAGATTT  GA
```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```
a122.pep
1  VVMIKIRNIH  KTFGKNTILR  GINLDVCKGQ  VVILGPSGS  GKTTFRLCLN
51  ALEMPEDGQI  EFDNERPLKI  DFSKKPSKHD  ILALRRKSGM  VFQYQNLFPH
101 KTALENVMEG  PVAVQGKPAA  QAREEALKLL  EKVLGDKVD  LYPYQLSGGQ
151 QQRVGIARAL  AIQPELMLFD  EPTSALDPEL  VQDVNLAMKE  LAREGWTMNV
201 VTHEIKFALE  VATTVVMDG  GVIVEQGSPK  ELFDHPKHER  TRRFLSQQIS
251 TKI*
```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFTGENTILRGIDLVDCKGQVVILGPSGSGKTTFRLCLNALEMPEDGQI					
a122	VVMIKIRNIHKTFTGKNTILRGINLDVCKGQVVILGPSGSGKTTFRLCLNALEMPEDGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSMVFQYQNLFPHKTALENVMEGPPAVQGKPAA					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSGMVVFQYQNLFPHKTALENVMEGPPAVQGKPAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
a122	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m122.pep	VQDVLDMKELAQEGWTMNVVTHEIKFALEVATTXVMDXGVIVEQGSPQDLFDHPKHER					
a122	VQDVNLAMKELAREGWTMNVVTHEIKFALEVATTVVMDGGVIVEQGSPKELFDHPKHER					
	190	200	210	220	230	240
	250					
m122.pep	TRRFLSQQSTKIX					

351

a122 |||||
 TRRFLSQIQSTKIX
 250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT
51  GCGCGGCATC GATTTGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCGCTGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG
201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC
301 GTGTTGGAAA ACGTGATGGA AGGCGCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTTTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGATAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG
451 CGTGTCGGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT
501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep

```

1  MIKIRNIHKT FGENTILRGI DLDVKGQVQV VILGPSGSGK TTFRLCLNAL
51  EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT
101 VLENVMEGPV AVQGKPAAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT
201 HEIKFTLEVA TNVVVMDGGV IVEQGSPEL FDHLKHERTR RFLSQIQAQ
251 I*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACTATTTT
51  GCGCGGCATC GATTTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAATCAGG CATGGTGTTT CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGGAAA ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG
451 CGCGTCGCA TCGCCCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT
501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG
551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTCGTTACG
601 CATGAAATCA AGTTCGCCTT AGAAGTGGCA ACCACGTCG TCGTGATGGA
651 CGGCGGCGTT ATTGTCAAC AAGGCAGCCC GCAAGATTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep

```

1  MIKIRNIHKT FGENTILRGI DLDVCKGQVQ VILGPSGSGK TTFRLCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT
201 HEIKFALEVA TTVVVMDGGV IVEQGSQDL FDHPKHERTR RFLSQIYSTK
251 I*

```

m122-1/g122-1 94.8% identity in 251 aa overlap

```

10      20      30      40      50      60
m122-1.pep  MIKIRNIHKTFGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF
          |||||
g122-1      MIKIRNIHKTFGENTILRGIDLDVKGQVQVILGPSGSGKTTFLRCLNALEMPEDGQIEF

```

352

	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
g122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTVLENVMEGPPVAVQGKPAAQA					
	70	80	90	100	110	120
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					
g122-1	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					
	130	140	150	160	170	180
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGSPPQDLFDHPKHERTR					
g122-1	DVLDTMKELAREGWTMVVVTHEIKFTLEVATNVVVMDGGVIVEQGSPPQDLFDHLKHERTR					
	190	200	210	220	230	240
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTCGGCAAAA ATACCATTTT
51  GCGCGGCATC AATTTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGGAAA ACGTGATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTGTGAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCGAGC ATTGGCGATT CAGCCCGAGC TGATGTTGTT
501 TGACGAACCC ACTTCCGCGC TTGACCCCGA GTTGGTGCAA GACGTGTGTA
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCGCGCT GGAAGTTGCC ACGACCGTTG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 CCAACACGA ACGGACGCGG AGATTTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT FGKNTILRGI NLDVCKGQVV VILGPSGSGK TFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLNAMKELA REGWTMVVVT
201 HEIKFALEVA TTVVVMDGGV IVEQGSPPKE FDHPKHERTR RFLSQIQSTK
251 I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGENTILRGIDLVDCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
	70	80	90	100	110	120
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					
m122-1	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					

q125.seq

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCGCCGCCA	TCGGGCTGGT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TCGCCCCCTT	GGGCTGGCAG	CGCGGTCTGG	CGGCCCTGCT	TTTGGGTTCAT
151	GCCGTCGGCG	GCGCGCTGTT	TTTTCGCGCG	GCGTATATCG	GCGCACTGAC
201	CGGACGCAGC	TCGATGGAA	GTGTGCGCCT	GTCGTTCCGG	AAATGCGGTT
251	CAGTGCCTGT	TTCGCTGGCG	AATATGCTGC	AACCTGGCCG	CTGGACGGCG
301	GTGATGATTT	ACGTTCGGCG	AacggTCAGC	TCCGCTTTGG	GCAAAGTGTT
351	GTGGGACggc	gaATCCTTTG	TCTGGTGGGC	ATTGGCAAAC	GCGCACTGA
401	TCGTGCTGTG	GCTGGTTTTC	GGCGCACGCA	GAACGGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	GCTTGCCGTG	TGTGTTTGA	GCGTCGAAGT
501	GTTTCGCTTCG	TCCGGCACAA	ACGCCGCGCG	CGCCGTTTCA	GACGGCATGA
551	CCTTCGGAAC	GGCAGTCCAA	CTGTCCGCCG	TCATGCCGCT	TTCCTGGCTG
601	CCGCTAGGCCG	CCGACTACAG	GCGCCAAGCA	GCGCCGCCGT	ATGCGGCAAC
651	CCTGACGGCA	ACGCTCGCCT	ATACGCTGAC	GGCGTCTGG	TTGTATGCCT
701	TGGGTTTGGC	GGCGGCTCTG	TTTACCGGAG	AAACCGACGT	GGCGAAAATC
751	CTGTTGGGCG	CGGGCTTGGG	CATAACGGGC	ATTCTGGCAG	TCGTCTCTC
801	CACCGTTACC	ACAACGTTTC	TCGATACCTA	TCCGCCCGGC	GCGAGTGCGA
851	ACAACATTTT	CGCGCGTTTT	GCGGAAATAC	CCGTCGCTGT	CGGCGTTACC
901	CTGatccgca	ccgtgcttgc	cgtcatgtcg	cccgttaccg	aatataaaaa
951	cttctctgctg	cttatccgct	cggatatttg	gccgatggcg	ggtggttttg
1001	attgcccgaCT	TTTttgtctt	AAAACGGCGT	GA	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 459>:

m125.seq

1	ATGTCGGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCTCCGCCA	TCGGGCTGAT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TTGCGCCTTT	GGGCTGGCAG	CGCGGTCTGG	CGGCTCTACT	TTTGGGT CAT
151	GCCGTTCGGC	GCGCGCTGTT	TTTTGCGGGC	GCGTATATCG	GCGCACTGAC
201	CGGACGCAAG	TCGATGAAA	CGGTGCGCCT	GTCGTTCCGG	AAACGCGGTT
251	CAGTGCTGTT	TTCCGTGGCG	AATATGCTGC	AAGTGGCCGG	CTCGACGCGC
301	GTGATGATTT	ACGCCGGCGC	AACGGTCAGC	TCCGCTTTGG	GCAAAGTGTT
351	GTGGGACGGC	GAATCTTTTG	TCGTGTGGGC	ATTGGCAAAC	GGCGCGCTGA
401	TTGTGCTGTG	GCTGGTTTTG	GGCGCACGCA	AAACAGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	GTTGGCGGTT	CTGTGGCTGA	GTGCCGAAGT
501	CTTTTCCACG	GACGAGCA	GCGCCGCACA	CGTTTCAGAC	GGCATGAGTT
551	TCGGAACGGC	AGTCGAGCTG	TCCGCCGTGA	TGCCGCTTTC	CTGCGTCCG
601	CTTGCCGCCG	ACTACACGCG	CCACGCGCGC	CGCCCGTTTG	CGGCAACCCT
651	GACGGCAACG	CTCGCCTACA	CGCTGACCGG	CTGCTGGATG	TATGCCCTTG
701	GTTTGGCAGC	GGCGCTTGTT	ACCGGAGAAA	CCGACGCTGC	AAAAATCCTG
751	CTGGGCGCAG	GTTTGgGTGC	GGCAGGCATT	TTGGCGGTGC	TCCTCTCCAC
801	CGTTACACACA	ACGTTTTCTCG	ATGCCTATTC	CGCCGGCGCG	AGTGCGAAC

851 ACATTTCCTG GCGTTTTGCG GAAACACCCG TCGCTGTCrG CGTTACCCCTG
 901 ATCGGCACGG TACTTGCCGT CATGCTGCCC GTTACCGAAT ATGAAAACCTT
 951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCGGgC GGTTTTGATT
 1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

m125.pep
 1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
 101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
 151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
 201 LAADYTRHAR RPFATLTAT LAYTLTGCWM YALGLAAALF TGETDVAKIL
 251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL
 301 IGTVLAVMLP VTEYENFLLI IGSVFAPMAG GFDCLFRLE TA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

m125/g125

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQORGLAALLLGHAVGGALFFAA					
	: : : : : : : : : :					
g125	MSGNASSPSSAAIGLVWFGAAVSIAEISTGTLLAPLGWQORGLAALLLGHAVGGALFFAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m125.pep	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
	: : : : : : : : :					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVGVATVSSALGKVLWDG					
	70	80	90	100	110	120
	130	140	150	160	170	179
m125.pep	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
	: : : : : : : : :					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	180
	180	190	200	210	220	230
m125.pep	DGMSFGTAVELSAVMPLSWPLAADYTRHARRPFAATLTATLAYTLTGCWMYALGLAAAL					
	: : : : : : : : :					
g125	DGMTFGTAVELSAVMPLSWPLAADYTRQARRPFAATLTATLAYTLTGCWMYALGLAAAL					
	190	200	210	220	230	240
	240	250	260	270	280	290
m125.pep	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
	: : : : : : : : :					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDYSAGASANNISARFAEIPVAVGVT					
	250	260	270	280	290	300
	300	310	320	330	340	
m125.pep	LIGTVLAVMLPVTEYENFLLIIGSVFAPMAGGFDCLFRLETAX					
	: : : : : : : : :					
g125	LIRTVLAVMLPVTEYKNFLLIIRSVFGPMAGGFDCLFCLKTAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

a125.seq
 1 ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC
 101 TTGCGCCTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTGCT TTTGGGTCAT

355

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151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCCGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTT GCGGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCCACG GCAGGCAGCA CCGCCGCACA GGTTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCGCTTTC TTGGCTGCCG
601 CTGGCCGCCG ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCC
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GCGTTGTTC ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAG GTTTGGGTGC GGCAGGCATT TTGGCGGTCG TCCTGTGCGAC
801 CGTTACCACC ACTTTTCTCG ATGCCTACTC CGCCGCGGTA AGTGCCAACA
851 ATATTTCCGC CAAACTTTTC GAAATACCCA TCGCCGTTGC CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCCG GTTACCGAAT ATGAAACTT
951 CTTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCG.GC GGTTTTGATT
1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1  MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
51  AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RPPAATLTAT LAYTLTGCMW YALGLAAALF TGETDVAKIL
251 LGAGLGAAGI LAVVLSTVTT TFLDAYSAGV SANNISAKLS EIPIAVAVAV
301 VGTLLAVLLP VTEYENFLLL IGSVFAPMAX GFDCRLFRLE TA*

```

m125/a125 95.6% identity in 342 aa overlap

```

m125.pep      10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
|
a125           10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA

m125.pep      70      80      90     100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
|
a125           70      80      90     100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG

m125.pep     130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
|
a125          130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD

m125.pep     190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF
|
a125          190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF

m125.pep     250     260     270     280     290     300
TGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
|
a125          250     260     270     280     290     300
TGETDVAKILLGAGLGAAGILAVVLSTVTTTFLDAYSAGVSANNISAKLSEIPIAVAVAV

m125.pep     310     320     330     340
IGTVLAVMLPVTEYENFLLIGSVFAPMAGGFDCRLFRLETAX
|
a125          310     320     330     340
VGTLLAVLLPVTEYENFLLIGSVFAPMAXGFDCRLFRLETAX

```

310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
1   AtgccgctcTG AAaccCcaaaa ggcACGCCGC CGGCTTTTCAG ACGGCATCGC
51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101 CTTTCCCTTC GCGGCTGCTg ctcggcacgG cggcctacCC GACCCCTGAA
151 ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201 GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTTGGT
251 CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301 CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351 TGAAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401 AGCCGGACGT GTTCCAACCTC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451 GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501 CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551 GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601 CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651 CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701 CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751 CTCGCCGTCG AATCCGACG GCTGGCATTG GAAGCCGGGC CGGTCGAAGC
801 GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTTTGC
851 ATTCGGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
1   MPSETPKARR RLSDGIASDN HTKESIMLTL YGETFPSRL L LGTAAYPTPE
51  ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLLQETG VPVLPNTAGC
101 QSVQEAHTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAEEILIKD
151 GFKVLPYCTE DLIACRRLLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201 RLPDTPLIID AGLGLPSQAA QVMEWGFQDV LLNTAVSRSG DPNVMARAFA
251 LAVESGR LAF EAGPVEARTK AASTPTVGQ PFWHSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
1   ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCC GAAATCCTCA
101 AACAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151 CGCGCGGGAA GCGGCGGCGA GGCGCACGGT CAGGGGTTTT GGTGCTGCTG
201 TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGG TGCCAAAGCG
251 TGCAGGAAGC GGTAACGACG GCGCAAATGG CGCGCGAAGT GTTTGAAACC
301 GATTGGATAA AATTGGAAC TATCGGAGAT GACGACACCT TGCAGCCGGA
351 TGTGTTCCAG CTTGTCGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401 AAGTGTGCTC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451 GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCGGA TCGGCACGGG
501 TTTGGGCGCG GTTCACGCCT ACGCGTTGAA CGTCCTGCGC GAACGCCTGC
551 CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601 GCACAAGTGA TGGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651 TTCCCGCAGC GGCGATCCGG TCAATATGGC ACGCGCCTTC GCACTCGCCG
701 TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTCGA AGCACGCGAC
751 AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GGCATTCCGG
801 GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
1   ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
51  RAGSGGEAHG QGFWSLLQET GVPVLPNTAG QSVQEAHTT AQMAREVFET
```

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```

101   DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRL
151   DAGCQALMPW AAPIGTGLGA VHAYALNVLR ERLPDTPLII DAGLGLPSQA
201   AQVMEWGFDG VLLNTAVSRS GDPVNMARAF ALAVESGRLA FEAGPVEARD
251   KQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep                      HYTKPEIMLTLYGETFPSRLLLGTAAYPTPEILKQSIQTAQ
                                ::||| ||||| ||||| ||||| ||||| ||||| ||||| ::|||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSRLLLGTAAYPTPEILKQSVRTAR
                                10      20      30      40      50      60

                                50      60      70      80      90      100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
              ||||| ||||| ::| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
              70      80      90      100      110      120

                                110      120      130      140      150      160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
              130      140      150      160      170      180

                                170      180      190      200      210      220
m126.pep      APIGTGLGAVHAYALNVLRERLPDTPPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
              ||||| ||||| ::| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRERLPDTPPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
              190      200      210      220      230      240

                                230      240      250      260      270
m126.pep      DPVNMARAFALAVESGRLA FEAGPVEARDKQASTPTVGQPFWHSAEYX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMARAFALAVESGRLA FEAGPVEARTKQASTPTVGQPFWHSAEYX
              250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

```

a126.seq
1   TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCCT TCGCGGCTGC TGCTCGGCAC AGCCGCCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACCGCCC GGCCCGCGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CCGCGGCGAG GCGCACGGTC AGGGGTTTGT
201 GTCGCTGCTT CAAGAAACCG GCGTTCCCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAACTC ATCGGCGACG ACGACACCTT
351 GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC GCGCGAAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCGGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCTA CGCGTTGAAC GTCCTGCGCG
551 AACGCTGCC CGACACGCCG CTGATTATCG ACGCGGGCTT GGGTTTGCCC
601 TCACAGGCGG CACAAGTGAT GGAATGGGGC TTTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCCTTCG
701 CACTCGCCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGCAAGC CAGCACGCCG ACAGTCGGAC AACCGTTTTG
801 GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
  1  LLIHYTKEPI MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
 51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101  FETDWIKLEL IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR
151  RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201  SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251  ARDKAQASTP TVGQPFWHS A EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

              10      20      30      40      50
m126.pep      HYTKEPIMLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE
              |||||
a126           LLIHYTKEPIMLTLYSETFPSRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE
              10      20      30      40      50      60

              60      70      80      90      100     110
m126.pep      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              |||||
a126           AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              70      80      90      100     110     120

              120     130     140     150     160     170
m126.pep      VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALN
              |||||
a126           VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALN
              130     140     150     160     170     180

              180     190     200     210     220     230
m126.pep      VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG
              |||||
a126           VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG
              190     200     210     220     230     240

              240     250     260     270
m126.pep      RLAFEAGPVEARDKAQASTPTVGQPFWHS A EYX
              |||||
a126           RLAFEAGPVEARDKAQASTPTVGQPFWHS A EYX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
  1  ATGCTCACCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
 51  GGCCGCGTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCC
101  GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151  GCGCACGGTC AGGGGTTTGT GTGCTGCTT CAAGAAACCG GCGTTCCCGT
201  CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251  CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301  ATCGGCGACG ACGACACCTT GCAGCCGGAC GTGTTCCAAC TCGTCGAAGC
351  GCGGGAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401  AAGACCTGAT TGCTTCCGCG CGCTGCTCG ATGCGGGCTG TCAGGCGTTG
451  ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCA
501  TCGGCTCAAA ATCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551  ACGCGGGCTT GGGTTTGCCT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601  TTTGACGGCG TATTGTTAAA CACCGCGCTT TCCCGCAGCG GCGACCCCGT
651  CAACATGGCG CGCGCCTTCG CACTCGCGGT CGAATCCGGA CGGCTGGCAT
701  TTGAAGCCGG GCCGGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751  ACAGTCGGAC AACCGTTTGT GCATTCGGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
  1  MLTLYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRTGCGGE
```

```

51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWWSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

```

m126-1.seq
1 ATGCTCACCC TATACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 GGCTGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAACCTC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCACG TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGTGCTT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CCGCCCCGAT CGGCACGGGT TTGGCGCGCG TTCACGCCCTA
501 CCGCTTGAAC GTCCTGCGCG AACGCTGCCG CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCG TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CCGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

```

m126-1.pep
1 MLTLYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTLYGETF	PSRLLLGTAAYPT	PEILKQSIQTAQPAMITV	SLRRAGSGGE	AHGQGFWSLL	
g126-1	MLTLYGETF	PSRLLLGTAAYPT	PEILKQSVRTARPAMITV	SLRRTGCGGE	AHGQGFWSLL	
	70	80	90	100	110	120
m126-1.pep	QETGVPVLPNTAGCQSVQEA	VTTAQMAREVFETDWIKLEL	IGDDDTLQPDVFQVLEAAEI			
g126-1	QETGVPVLPNTAGCQSVQEA	VTTAQMAREVFETDWIKLEL	IGDDDTLQPDVFQVLEAAEI			
	130	140	150	160	170	180
m126-1.pep	LIKDGFKVLPYCTEDLIACR	RLLDAGCQALMPWAAPIGTGLGAVHAYALN	VLRERLPDTP			
g126-1	LIKDGFKVLPYCTEDLIACR	RLLDAGCQALMPWAAPIGTGLGAVHAYALK	ILRERLPDTP			
	190	200	210	220	230	240
m126-1.pep	LIIDAGLGLPSQAAQVMEWG	FDGVLLNTAVSRSGDPVNMA	RAFALAVESGRLAFEAGPVE			
g126-1	LIIDAGLGLPSQAAQVMEWG	FDGVLLNTAVSRSGDPVNMA	RAFALAVESGRLAFEAGPVE			
	250	260				
m126-1.pep	ARDKAQASTPTVGQPFWWSA	EYX				
g126-1	ARTKAQASTPTVGQPFWWSA	EYX				
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

```

a126-1.seq
1 ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 AGCCGCTTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGATG CCGCGGCGAG

```

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```

151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAACTC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

a126-1.pep

```

1  MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

	10	20	30	40	50	60
a126-1.pep	MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE AHGQGFWSLL					
	: : : : : :					
m126-1	MLTLYGETFP SRLLLGTAAY PTPEILKQSIQTAQPAMITV SLRRAGSGGE AHGQGFWSLL					
	10	20	30	40	50	60
a126-1.pep	70	80	90	100	110	120
	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
m126-1	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
	70	80	90	100	110	120
a126-1.pep	130	140	150	160	170	180
	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	190	200	210	220	230	240
	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	250	260				
	ARDKAQASTP TVGQPFWWSA EYX					
m126-1	ARDKAQASTP TVGQPFWWSA EYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

1  ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCAGATACG
51  CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GGCGGTTTTT GGTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GGCGCAAATT CAAACGCTGG
251 CTTTGTGCGT GTTTGCGGTG GCGGCGGCGG TCGTCTGGC GACAAAAGAA
301 CTGATTATGT GTCGTGCGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA

```

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```

551 CGGTCGAAAT CCCC GTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCACGCCCG
701 CCGCCAGGCC GCGCGTTACC CGCGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCCTC CCCC GTTTCA AAGCGGCTGG AAATCCAACA
801 GCGCGTTATG GACGAATTTT TCGCGGTACA ATACCGCCTG TTAAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

```

g127.pep
1  MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLLNI HFRRHPDFGI
51  ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAADV VATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVs KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

```

m127.seq
1  ATGGAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51  TCGGAGGCG GTCGAATCCG TGGCGGCGGT TCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGCGTTTTC GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCGAAATC CAAACGCTGG
251 CTTTGTGCGAT GTTTGCGGTG GCGGCGGCGG TCGTCGTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCGGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGACAGC TTGCGGGAAC CACCGTTTCT TCCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA
551 CCGTCGAAAT CCCC GTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGgAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCACGCCCG
701 CCGCCAGACC GCGCGTTACC CGCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCC GTTTCA AAGCGGCTGG AAATCCAACA
801 GCGCGTTATG GACGAATTTT TCGCGGTACA ATACCGCCTG TTAAATCACC
851 CCGCCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

```

m127.pep
1  MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLLNI HFKRHPDFGI
51  ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAADV VATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVs KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

```

m127/g127
          10      20      30      40      50      60
m127.pep  MEIWNMLDTWLGAVPIRAEAVESVAAVAALLLARALLLNIHFKRHPDFGIESKRRFLVAS
          |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
g127       MEIWNMLNTWPDVPIRAEAAESVAAVAALLLARALLLNIHFRRHPDFGIESKRRFLVAS
          10      20      30      40      50      60

          70      80      90     100     110     120
m127.pep  RNITLLLVLFSLAFIWSAQIOTLALSMFAVAAADV VATKELIMCLSGSILRSATQQYSVG
          |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
g127       RNITLLLVLFSLAFIWSAQIOTLALSMFAVAAADV VATKELIMCLSGSILRSATQQYSVG

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

```

a127.seq
1  ATGGAAATAT  GGAATATGTT  GGACACTTGG  CTCGGTGCCG  TCCCAGATACG
51  TGC GGAGGCG  GTCGAATCCG  TGGCGGTGGT  CGCGGCTTTG  CTGCTGGCGC
101 GCGCCCTTCT  GTTGAATATC  CACTTCAAAC  GGCATCCGGA  TTTCGGCATC
151 GAAAGCAAGC  GGC GGTTTTT  GGTGGCCAGC  CGCAATATAA  CGCTGCTTTT
201 GGTGCTGTTT  TCGCTGGCAT  TTATCTGGTC  GGCGCAAATC  CAAACGCTGG
251 CTTTGTCGAT  GTTTGCGGTG  GCGGCGGCGG  TCGTCGTGGC  GACGAAGGAA
301 CTGATTATGT  GTCTGTCGGG  CAGCATTTTA  AGGTCTGCCA  CCCAGCAATA
351 CTCGGTCGGC  GACTATATCG  AAATCAACGG  CCTGCGCGGG  CGCGTGGTCG
401 ACATCAACCT  GTTGAACACG  CTGATGATGC  AGGTGCGTCC  GAACCCCTTG
451 GTCGGACAGC  TTGCGGGAAC  CACCGTTTCT  TTCCCAACA  GCCTGTTGTT
501 GAGCCACCCC  GTGCGCGCGG  ACAATATTTT  GGGCGACTAC  GTCATCCATA
551 CGGTCGAAAT  CCCGGTTCCC  ATCCATTTGG  ATTCGGATGA  AGCCGTATGC
601 CGTCTGAAAG  CCGTACTCGA  GCCCTTGTGC  GCGCCCTACA  TCCCCGCCAT
651 CCAACGGCAT  TTGGAACACG  TGCAGGCGGA  AAAACTGTTT  ATCACGCCCC
701 CCGCCAAACC  GCGCGTTACC  CGCGTGCCGT  ACGATGACAA  GGCATACCGC
751 ATCATCGTCC  GCTTCGCCTC  CCCC GTTTCA  AAGCGGCTGG  AAATCCAACA
801 GCGCGTTATG  GACGAATTTT  TCGCGGTACA  ATACCGCCTG  TTAAATTACC
851 CCGCCGCTC  CGAAACACTT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

```

a127.pep
1  MEIWNMLDTW  LGAVPIRAEA  VESVAVVAAL  LLARALLLNI  HFKRHPDFGI
51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAAVVVATKE
101 LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151 VGQLAGTTVS  FPNSLLLSHP  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201 RLKAVLEPLC  APYIPAIQRH  LENVQAEKLF  ITPAAKPRVT  RVPYDDKAYR
251 IIVRFASPV  KRLEIQQAVM  DEFLRVQYRL  LNYPAGSETL  *

```

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLLNIHFKRHPDFGIESKRRFLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLLNIHFKRHPDFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAAKPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNYPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

1	atgattgaca	acgCActgct	ccacttgggc	gaagaaccCC	GTTTaatca
51	aatccaaacc	gaagACAtca	AACCCGCCGT	CCAAACCGCC	ATCGCCGAAG
101	CGCGCGGACA	AATCGCCGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTCGTG	TCCCATCTCA	ACTCCGTCGT	CGACACGCCC	GAACGCGCGC
251	CCGTCTATAA	CGAACTGATG	CCTGAAATCA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAACTGTA	CAACCGCTTC	AAAACCATCA	AAAAATCCCC
351	CGAATTTGCA	ACGCTTTCCC	CCGCACAAAA	AACCAAGCTC	GATCAGGACC
401	TGCGCGATTT	CGTATTGAGC	GGCGCGGAAC	TGCCGCCCCG	ACGCGAGGCA
451	GAACCTGGCAA	AACTGCAAAC	CGAAGGCGCG	CAACTTTCCG	CCAAATTTCT
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTTAC	TTTGACGATG
551	CCGACCCGCT	TGCCCGCATT	CCCGAAGACG	CGCTCGCCAT	GTTTGCCGCC
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTACCTT	GCCGTTATCC	AATACGCCGG	CAACCGCGAA	CTGCGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGTGCCA	GCGAACTTTC	AAACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA
801	AACCGccaaa	cTGCTCGGCT	TTAAAAATTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAGGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCGCCGCG	CCAAACCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCCG	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA
1001	GCTACGCCGG	CGAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTTCTGGCAG	GCTTGTTTCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	CGCCGAAAAA	ACCGTTCCCC
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGGCGGCG	TTTATATGGA	TTTGTACGCA	CGCGAAGGCA	AACGCGGCGG
1251	CGCGTGGATG	AACGActaca	AAGGCCGCCG	CCGCTTTGCC	GACGgcacGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCGTCGGC
1351	GGCAAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCCTCACCC	TCTTCCACGA
1401	AacCGGCCAC	GGACTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAACGggcGC
1451	TGTCCGGCAT	CAAcggcgtA	GAATGGGACG	CGGTCGAACT	GCCCAGCCAG
1501	TTATATGGAA	ACTTCGTTTG	GGAATACAAT	GTATTGGCAC	AAATGTCCGC
1551	CCACGAAGAA	AccgGCGAGC	CCCTGCCGAA	AGAACTCTTC	GACAAAAATGC
1601	TcgcCGCCAA	AAACTTCCAG	CGCGGTATGT	TCCTCGTCCG	GCAAAATGGAG
1651	TTCGCCCTCT	TCGATATGAT	GATTTACAGT	GAAAGCGACG	AATGCCGTCT
1701	GAAAAAACTGG	CAGCAGGTTT	TAGACAGCGT	GCGCAAAGAA	GTcGCCGTCA
1751	TCCAACCGCC	CGAATACAAC	CGCTTCGCCA	ACAGCTTCGG	CCacatctTC
1801	GCcggcGGCT	ATTCCGAGG	CTATTACAGC	TACGCATGGG	CCGAAGTCct
1851	cAGCACCGAT	GCCTACGCCG	CCTTTGAAGA	AAGcGACGac	gtcGCCGCCA
1901	CAGGCAAACG	CTTCTGGCAA	GAAAtccttg	ccgtcggcgg	ctCCCCGAGC
1951	gcgGCGGAAT	CCTTCAAAGC	CTTCCGCGGA	CGCGAACC GA	GCATAGACGC

2001 ACTGCTGCGC CAAagcggtT TCGACAACGC gGcttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

```

gl28.pep
  1 MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTTGWA
 51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY PDAAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAFAEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

```

m128.seq (partial)
  1 ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
 51 AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGTAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCG GAACGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAAA AACCAAACTC AACCAC
  1 TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
 51 wGTCAAAAAA TAyTTCCcyG TCGGCAAwGT ATTAACGGA CTGTTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGTC
151 TGGCACAAG ACGTGCCTA TtkTGAATTG CAACAAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTTCTG CCGCACGCTG
301 CAAYTGCCCA CCGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTaka ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CGGCATGTTC yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCTATC
751 CAGCCGCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

```

m128.pep (partial)
  1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTTGWA
 51 NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH
//
  1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTPPV
 51 WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFS DGTL
101 QLPTAYLVCN FAPPVGGREA RLSDHEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT

```

365

301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHSGF DNAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQTHGTWANTVERLTGIT					
	: :					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
	:					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLGSAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	:					
m128	TLSPAQKTKLNH					
	130					
	//					
			340	350	360	
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
	:					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
			10	20	30	
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
	:					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
	:					
m128	GRRRFSGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSESDCRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
	:					
m128	XVRQXEFALFDMMIYSEDDEGRLLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
	: :					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSRGAESFKAFRGREPS					
	280	290	300	310	320	330

366

	670	679
g128.pep	IDALLRQSGFDNAA	X
	: :	
m128	IDALLRHSFGDNAV	X
	340	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1   ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTAC CGACACGCCC GAACGCGCGG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAACCTC AACCACGATC
401 TGCGCGATTT CGTCCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCGG CCAAATCTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTGACAA ACACGCCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTTCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCAGACAC GGCTGACACC ACCTGCTTAC CCAAGTCGAC GAATGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAAC GCCCAGTCAG
1501 TTTATGGAAT ATTTCGTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 TAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTGC
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCGCGGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1   MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWGA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEI SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTFPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGR LKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep	-----					140
						150
a128	ARRAKPYAEKDLAEVKAFARESGLGLADLPWDLG YAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPV VWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPV VWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTTFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWD AVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWD AVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

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```

          400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAESFKAFRG
          610      620      630      640      650      660

          460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 487>:

g128-1.seq (partial)

```

1  ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACGCTTTCCC CGGCACAAAA AACCAAGCTC GATCACGACC
401 TGCGCGATTG CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACC CGCAAA TGTCTCGGCT TTA AAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCGC CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAACACCTCG GTCTCGCCGA CCCGACGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTCGC
1101 CCAAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTGCTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGCGAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG EEPRFNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQNGKKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV K

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 489>:

m128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGCG GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG

```

```

201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACACGATC
401 TGCGCGATTT CGTCTCAGC GCGCGGAAC TGCCGCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 ACACTACCTC GCCGTATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGCG GGACACGCCC GAACAAGTTT TAAACTTCTT GCACGACCTC
901 GCCCGCGCG CCAAACCCTA CGCCGAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAAATG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAGTCGAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCGC
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACAA AGAGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CCGGTGGATG AACGACTACA AAGGCCGCG CCGTTTTTCA GACGGACGCG
1301 TGCAACTGCC CACCGCCTAC CTGCTCTGCA ACTTCGCCCC ACCCGTCGGC
1351 GGCAGGGAAG CCCGCCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCAGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CGTTCGAACT GCCAGCCAG
1501 TTTATGGAAT ATTTCTGTTT GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCGCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGGCCAA AAATCTCAA CGCGGCATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAA GTGCGCGTCA
1751 TCCAGCCGCC CGAATACAAC CGCTTCGCTT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGC CCTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGC CGGAACCGA GCATAGACGC
2001 ACTCTTGGC CACAGCGGT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGW
51 NTVEPLTGIT ERVGRIVGVV SHLSNVADTP ELRAVYNELM PEITVFFTEI
101 QDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLALALQTA LGLFKNYAEL SLATKMDATP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLKNW QQVLDSVRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAERG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pep MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
g128-1.pep ERVGRIVGVVSHLSNVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      ERVGRIVGVVSHLSNVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

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	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAE	LAKLQTEGAQLSAKFSQNVLDATDAFGIY				
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSESKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDL	SYAGEKLREAKYAFSETEVKKYFPVGK				
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVVGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVVGREARLSHDEILILFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGCGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACGCCC ATTGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAGCCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCAGGATC
401 TGCGCGATTT CGTCCTCAGC GCGCGCGAAC TGCCGCCCCG ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTCCG CCAAATCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCGCA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCGCG CGAAAAATG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCGC
1101 CCAAAATCAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGCGGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG

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1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTCGTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGGAACCGA GCATAGACGC
2001 ACTCTTGC GC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELEPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLEKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AESFKAFRG REPSIDALLR HSGFDNAA*

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m128-1/a128-1 97.8% identity in 677 aa overlap

```

10 20 30 40 50 60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
|||||
m128-1 MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
10 20 30 40 50 60

70 80 90 100 110 120
a128-1.pep ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||:|||||:|||||
m128-1 ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
70 80 90 100 110 120

130 140 150 160 170 180
a128-1.pep TLSHAQKTKLNHDLRDFVLGSAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
|||
m128-1 TLSPAQKTKLNHDLRDFVLGSAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
130 140 150 160 170 180

190 200 210 220 230 240
a128-1.pep FDDAAPLAGI PEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
|||||:|||||
m128-1 FDDAAPLAGI PEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
190 200 210 220 230 240

250 260 270 280 290 300
a128-1.pep TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
|||||
m128-1 TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
250 260 270 280 290 300

310 320 330 340 350 360
a128-1.pep ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
|||||:|||||

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m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
              310      320      330      340      350      360

a128-1.pep  VLNGLFAQIKKLYGIGFTEKTPVWVKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420
|||||
m128-1      VLNGLFAQIKKLYGIGFTEKTPVWVKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420

a128-1.pep  NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
              430      440      450      460      470      480
|||||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
              430      440      450      460      470      480

a128-1.pep  ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540
|||||
m128-1      ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

a128-1.pep  RGMFLVRQMEFALFDMMIYSEDDEGRKLNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
              550      560      570      580      590      600
|||||
m128-1      RGMFLVRQMEFALFDMMIYSEDDEGRKLNWQQVLDVSRKVKAVIQPPEYNRFALSFGHIF
              550      560      570      580      590      600

a128-1.pep  AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660
|||||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

a128-1.pep  REPSIDALLRHSGFDNAAX
              670      679
|||||
m128-1      REPSIDALLRHSGFDNAAX
              670

```

a128-1/ P44573

```

sp|P44573|OPDA_HAEIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlC) homolog
- Haemophilus influenzae (strain Rd KW20)
>gi|1573174 (U32706) oligopeptidase A (prlC) [Haemophilus influenzae Rd] Length = 681
Score = 591 bits (1507), Expect = e-168
Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

```

```

Query: 4   NALLHLGEEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXXTHGTWANTVEPLTGITERV 63
          N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5   NPLLNIIQGLPPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64  GRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFDTLS 123
          R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65  NRAWSPVSHLNSVKNSTELREAYQTCLPLLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124 HAQKTKLNHDLRDFVLSGAELPPEQQABLAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
          AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125 IAQKKAIEENSLRDFELSGIGLSEKQQRYSGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYVTRA 243
          A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA
Sbjct: 185 EAELAGLPESALQAAQQAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

Query: 244 SELSDD-GKFDNTANIDRTLLENALQTAKLGLGPKNYAELSLATKMATDTPQVLNFLHDLAR 302
          SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245 SEQGPNAGKWDNSKVMEEILTLRVELAKLLGFNTYTELSLATKMAENPQQVLDFLDHLAE 304

Query: 303 RAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGKVL 362
          RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFP +V+
Sbjct: 305 RAKPQGEKELQELKGYCEKEFGVTLELPWDIGFYSEKQKQHLVAINDEELRPYFPENRVI 364

```

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNGETIGGVYMDLYAREGKRGGAWM 420
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGGAWM
 Sbjct: 365 SGLFELIKRIFNIRAVRKGVDTWKDVRFDLIDENDQLRGSFYLDLYAREHKRGGAWM 424

Query: 421 NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXQVD 480
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D
 Sbjct: 425 DDCIGRKRKLDGSIETFPVAYLTCNFNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSINGVWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ
 Sbjct: 485 VSDVAGINGVPWDAVELPSQFMENWCWEEELAFISGHYETGEPLPKEKLTQLLKAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDSVRKEVAVVRPEYNRFANSFGHIF 600
 MF++RQ+EF +FD ++ D + L SV+ +VAV++ ++ R +SF HIF
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNQILDTLKSVKSQVAVIKGVDWARAPHFSHFIF 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAPFEESDDV-AATGKRFWQEILAVGGSRAAESPKAFR 659
 WAEVLSADAY+ FEE TGK F EIL GGS E FK FR
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGSEEPMELFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676
 GREP +DALLRH G N
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq
 1 ATGCTTTTCAC CTCCTCGGCG TAAAACGGCG GCACATCAAT CAAGCCGTCT
 51 TTCATTTGCG TGCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAAATCAAT
 101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG
 151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT
 201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GGCGGTGCGA TCCTGTTTCA
 251 TCCGGACAAA CGCGTTGGCA GTCGGAAT CCGCCCGGCC GTGTCAAATA
 301 ATGCGTTACT TTGCCCGGCT CTGTCTCTTT GTAAGCGGCG GTCTTTTTTT
 351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC
 401 AATCAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG
 451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGGCAT TTAGCCGGT
 501 AACTTGA

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep
 1 MLSPPRRKTA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT
 51 PTAAAVHPYP RFRHLPPQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
 101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
 151 TYRAGFCLSD LAAFRPVT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)
 1 ..TATCTGCGCT TCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
 51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
 101 GAAAATTCGG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
 151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCG GTTATCCCCA TCTGTTTGAG
 201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTTCAT
 251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCGCTA
 301 TCCGATTTGA CGGCATTTAG ACCGGTAACT TGA

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)
 1 ..YLRPHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
 51 FVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL
 101 SDLTAFRPVT *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

```

                                10      20      30
m129.pep                      YLRFHYLPFQAAGIGTEQVAVKSCFIQINT
                                | | | : | | | | | | | : | | | : | | | : | :
g129      RDQNQYRAASSPNRGLPRFPITPTAAAVHPYPRFRHLPFQAAGIGAEQAAVESCIRTNA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m129.pep      LVVGKFGRLCQIMRYFGRVLFVSGGLFLRVIPICLSAXQMVAAVQSKCLAISCRXASGC
                | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g129      LAVGKSGRPCQIMRYFGRVLSFVSGGLFLRAIRICLGAWQTAAAVQSKCLAISCRQASGC
                90      100     110     120     130     140

                                100     110
m129.pep      CPTYXAGFCLSDLTAFRPVTX
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g129      RPTYRAGFCLSDLAARFPVTX
                150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

```

a129.seq (partial)
1  TATCTGCGCT TTCACTATTT GCCCTTTTCAG GCTGCGGGCA TAGGGACGGA
51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
101 GAAAATTCGG CCAGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCGC GTTATCCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTTAT
251 GCAGATAGGC ATCCTGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCGCTA
301 TCCGATTGA CGGCATTTAG ACCGGTAACT TGA

```

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

```

a129.pep (partial)
1  YLRFHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGQLC QIMRYFGRVL
51 FVSGGLFLR VIPICLSA*Q MVAAVQSKCL AISCR*ASWC CPTY*AGFCL
101 SDLTAFRPVT *

```

m129/a129 98.2% identity in 110 aa overlap

```

                                10      20      30      40      50      60
m129.pep      YLRFHYLPFQAAGIGTEQVAVKSCFIQINTLVVGKFGRLCQIMRYFGRVLFVSGGLFLR
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a129      YLRFHYLPFQAAGIGTEQVAVKSCFIQINTLVVGKFGQLCQIMRYFGRVLFVSGGLFLR
                10      20      30      40      50      60

                                70      80      90      100     110
m129.pep      VIPICLSAXQMVAAVQSKCLAISCRXASGCCPTYXAGFCLSDLTAFRPVTX
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a129      VIPICLSAXQMVAAVQSKCLAISCRXASWCCPTYXAGFCLSDLTAFRPVTX
                70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

```

g130.seq
1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51 TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG TGGATCGTTC GGCGATGTCG ATGCCACTAC GGAAGCGGCA
151 ACGCAGACCC GCATCCAGCC TGTCGACAAA TTGACGATGG GTGACGGCAT
201 CCCCCTCGGC GAACGCCAAG GCGAACAGAT TTTCCGCCAA ATCTGTATCC

```

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCTA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAAGTC AAACGGGCGA TTACCTACAT GGCGAATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGACAGT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
1 MKQLRDNKAQ GSALFTLVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAADLTQDEL KRAITYMANK
151 SGGSPNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVGDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACCGC
101 GTATCGgCAA GGCTTCGATA CCTTGTTCCTA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAAGTCTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGACAGT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACcCCC TGCGGTGCGC GTTGACGGTA AAAAAGTCTT CGAAGCAACC
401 TGTGAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCC GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACAA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAArG CGgCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQFDT LFQHALNGFN
51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAAPEAA KAEDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPAXG NAGLSDDEVK AAVDYMANQS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

m130/g130

```

m130.pep
10 20 30
GEQIFGKICIQCHAADSNVPNAPKLEHNGD
|||||
g130
50 60 70 80 90 100
DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD

40 50 60 70 80 89
XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTQDELKRAITYMANKSGGSFPNPDEAAP
|||||
g130
110 120 130 140 150 160
WAPRIAQGFDTLFQHALNGFNAMPAKGGAADLTQDELKRAITYMANKSGGSFPNPDEAAP

```

376

	90	100	110	120	130	140
m130.pep	ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
g130	ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130.pep	KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAAVDYMANQSGAKFX					
g130	KKDDWAPRIKKGKETLHKHALEGFNAMPKGGNAGLSDEVKAAVDYMANQSGAKFX					
	230	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCCT
51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG CGGCTCGTTC GGCATGTCG ATGCCACTAC GGAAGCAGCA
151 ACGCAGACCC GTATCCAGCC TGTCGGACAA TTGACGATGG GCGACGGCAT
201 CCCCGTCGGC GAACGCCAAG GCGAACAGAT TTTCCGCAAA ATCTGTATCC
251 AATGCCACGC GCGGCACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGATT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGTAG
401 ACCTGACCGA TCAGGAACTC AAACGGGCGA TTACTTACAT GGCGAACAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAAGTG TGCCACGGCG GTTCGATTCC
651 CCGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACACGCCC TTGAAGGCTT TAACGCGATG
751 CTGCCAAAG GCGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ GSALFTLVSG IVIVIAVLVF LIKLAGSGSF GDVDATTEAA
51  TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAVDLTDQEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

				10	20	30
m130.pep				GEQIFGKICIQCHAADS NVPNAPKLEHNGD		
a130	DATTEAATQTRIQPVGQLTMDGIPVGERQGEQIFGKICIQCHAADS NVPNAPKLEHNGD					
	50	60	70	80	90	100
	40	50	60	70	80	89
m130.pep	XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
a130	WAPRIAQGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
	110	120	130	140	150	160
	90	100	110	120	130	140
m130.pep	ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
a130	ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130.pep	KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAAVDYMANQSGAKFX					

|||||
a130 KKDDWAPRIKKGKETLHKHALEGFNAMPAGGNAGLSDDEVKAAVDYMANQSGAKFX
230 240 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

g132.seq
1 ATGGAAGCCT TCAAAACCCT AATTTGGATT ATTAATATTA TTTCCGCTTT
51 GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACCTT CCGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CCAACTTcct CAgccGCTCG AccGccGTTG CAGCAACAtt
201 tttcttTGca acctgcAtgg gctatggTgt atattcacac CCACACGACA
251 AAACACGGTT TGGACTTcag caacataCGA CAGACTCAGC AagcACCCAA
301 ACCcgtAAGC AATACCGAAC CTTCTGCCCC TGTTCTCAG CAGCAGAAAT
351 AACagtTTTT CAAATgccga caTGgtga

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

g132.pep
1 MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51 AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

m132.seq (partial)
1 ATGGAACCCT TCAAAACCTT AATTTGGATT GTTAATTTAA TTTCCGCTTT
51 GGCCGTCTTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGA...

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

m132.pep (partial)
1 MEAFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

m132/g132

	10	20	30	
m132.pep	MEPFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG			
	: : :			
g132	MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

a132.seq
1 ATGGAAGCCT TCAAAACCCT AATTTGGATT GTTAATATAA TTTCCGCTTT
51 GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CCGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CTAACCTCCT CAGCCGCTCG ACCGCCGTTG CAGCAACATT
201 TTTCTTTGCA ACCTGCATGg GCTATGGTGT ATATTCACAC CCACACGACA
251 AAACACGGTT TGGACTTCAG CAACGTACAA CAAACTCAGC AAGCACCCAA
301 ACCCGTAAGC AATACCGAAC CTTCTGCCCC TGTTCTCAG CAGCAGAAAT
351 AACAGTTTTT CAAATGCCGA CATGGTGA

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

a132.pep
1 MEAFKTLIWI VNIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51 AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QRTTNSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

m132/a132 92.1% identity in 38 aa overlap

378

	10	20	30	
m132.pep	MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG			
	: :			
a132	MEAFKTLIWIIVNIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

g134.seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCCAGTGCGG	GTAAACCAC	GCTGACCGAA	AAACTGCTGC
101	TGTTTTCGGG	CGCGATTCAA	AGCGCAGGCA	CGGTGAAAGG	TAAGAAAACC
151	GGCAAATTCG	CCACCTCCGA	CTGGATGGAC	ATCGAGAAGC	AGCGCGGCAT
201	TTCCGTGGCA	TCAAGCGTGA	TGCAGTTCGA	CTACAAAGAC	CACACCGTCA
251	ACCTCTTGGA	CACGCCGGGA	CACCAAGACT	TCTCCGAAGA	CACCTACCGC
301	GTTTTAACCG	CAGTGGACAG	CGCCTTGATG	GTCATCGACG	CGGCAAAAGG
351	CGTGAAGCG	CAAACCATCA	AACCTCTGAA	CGTCTGCCGC	CTGCGCGATA
401	CGCCGATTGT	TACCTTCATG	AACAAATACG	ACCGCGAAGT	GCGCGATTCT
451	TTGGAACCTCT	TGGACGAAGT	GGAAGACATC	CTGCAAAATC	GCTGCGCGCC
501	CGTTACCTGG	CCGATCGGTA	TGGGCAAAAA	CTTCAAGGGC	GTGTACCACA
551	TCCTGAACGA	CGAAATCTAT	CTCTTTGAAG	CGGGCGGCGA	ACGCCTGCCG
601	CACGAGTTCG	ACATCATCAA	AGGCATAAAC	AATCCCGAAT	TGGAACAACG
651	CTTCCGTTG	GAAATCCAGC	AGTTGCGCGA	CGAAATCGAA	TTGGTGCAGG
701	CGGCTTCCAA	CGAATTTAAT	CTCGacgaAT	TTCTCGccgG	CGAACTCACG
751	CCAGTGTCT	TCGGCTCTGC	GATTAACAAC	TTCGGCATT	AGGAAATCCT
801	CAATTCATTG	ATTGACTGGG	CACCCGCACC	GAAACCGCGC	GACGCGACCA
851	TGCGCATGGT	CGGGCCGGAC	GAGCCGAAAT	TTTCCGGATT	TATCTTTAAA
901	ATCCAAGCCA	ATATGGACCC	GAAACACCGC	GACCGTATCG	CCTTCTTGCG
951	CGTCTGCTCC	GGTAAATTCG	AGCGCGGCAT	GAAGATGAAA	CACCTGCGTA
1001	TCAACCGCGA	AATCGCCGCC	TCCAGCGTAG	TAACCTTCAT	GTCGCACGAC
1051	CGCGAACTGG	CGGAAGAAGC	CTACGCCGGC	GACATCATCG	GCATCCCGAA
1101	CCACGGCAAC	ATCCAAATCG	GCGACAGCTT	CTCCGAAGGC	GAACAATCTG
1151	CGTTTACCGG	CATCCCATTC	TTCGCGCCCG	AACTGTTCCG	CAGCGTCCGC
1201	ATCAAAAACC	CGCTGAAAAT	CAAACAACCTG	CAAAAAGGTT	TGCAACAACCT
1251	CGGCGAAGAA	GGTGCGGTTT	AAGTATTCAA	ACCGATGAGC	GGCGCGGATT
1301	TGATTTTGGG	TGCGGTCGGC	GTGTTGCAGT	TTGAAGTCGT	AACCTCACGC
1351	CTCGCCAACG	AATACGGCGT	GGAAGCCGTG	TTCGACAGCG	CATCCATCTG
1401	GTCGGCGCGC	TGGGTATCGT	GCGACGACAA	GAAAAAACTG	GCGGAATTTG
1451	AAAAAGCCAA	CGCAGGCAAC	CTCGCCATCG	ACGCAAGGCG	CAACCTCGCC
1501	TACCTCGCCC	CCAACCGCGT	GAATTTGGGG	TTGACGCAAG	AACGCTGGCC
1551	GGACATCGTG	TTCCACGAAA	CGCGCGAACA	TTCGGTCAAA	CTCTAA

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

g134.pep

1	MSQEILDQVR	RRRTFAIISH	PDAGKTLTE	KLLLFSGAIQ	SAGTVKGKKT
51	GKFATSDWMD	IEKQRGISVA	SSVMQFDYKD	HTVNLLDTPG	HQDFSEDYR
101	VLTAVDSALM	VIDAAKGVEA	QTIKLLNVCR	LRDTPIVTFM	NKYDREVRDS
151	LELLDEVEDI	LQIRCAPVTW	PIGMGKNFKG	VYHILNDEIY	LFEAGGERLP
201	HEFDIIKGIN	NPELEQRFPL	EIQQLRDEIE	LVQAASNEFN	LDEFILAGELT
251	PVFFGSAINN	FGIQEILNSL	IDWAPAPKPR	DATMRMVGPD	EPKFSGFIFK
301	IQANMDPKHR	DRIAPLRVCS	GKFERGMKMK	HLRINREIAA	SSVVTFMSSD
351	RELAEEAYAG	DIIGIPNHGN	IQIGDSFSEG	EQLAFTGIPF	FAPELFRSVR
401	IKNPLKIKQL	QKGLQQLGEE	GAVQVFKPMS	GADLILGAVG	VLQFEVVTSR
451	LANEYGVAV	FDSASIWSAR	WVSCDDKKKL	AEFEKANAGN	LAIDAGGNLA
501	YLAENRVNLG	LTQERWPDIV	FHETREHSVK	L*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

m134.seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCTGACGCAG	GTAAACCAC	GTTGACTGAA	AAACTCTTGC
101	TGTTTTCGGG	CGCGATTGAG	AGCGCGGGTA	CGGTAAAAGG	CAAGAAAACC
151	GGCAAATTCG	CCACTTCCGA	CTGGATGGAA	ATCGAGAAGC	AGCGCGGCAT


```

201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAAATG GTCATCGACG CGGCAAAAGG
351 CGTGGGAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAACTTT TGGACGAAGT GGAAAACATT TAAAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGAAATTTAT CTCTTTGAAG CTGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTTAAAT CTCGACGAAT TCCTCGCCGG CGAACTCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CGCCC GCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGGAC GAGCCGAAGT TTTCCGGATT TATCTTCAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGGC
951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TTACCTTCAT GTCGCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTGG
1151 CGTTCACCGG CATCCCATTC TTCGCACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACG CAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GGCGCGGTGC AGGTGTTCAA ACCGATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAACG AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAAGT GCTGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACGCGT GAATTTGGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

m134.pep

```

1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKID NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

m134/g134

```

          10      20      30      40      50      60
m134.pep MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
|||||
g134      MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
          10      20      30      40      50      60

          70      80      90     100     110     120
m134.pep IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAKGVEA
|||||
g134      IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAKGVEA
          70      80      90     100     110     120

          130     140     150     160     170     180

```

380

m134 . pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVENILKIRCAPVTWPIMGKNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVEDILQIRCAPVTWPIMGKNFKG
	130 140 150 160 170 180
m134 . pep	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134 . pep	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPDPEPKFSGFIFK
	250 260 270 280 290 300
m134 . pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELAEEAYAG
	310 320 330 340 350 360
m134 . pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134 . pep	GAVQVFKPMSGADLILGAVGV LQFEVVTSRLANEYGV EAVFDSASIWSARVWSCDDKKKL
g134	GAVQVFKPMSGADLILGAVGV LQFEVVTSRLANEYGV EAVFDSASIWSARVWSCDDKKKL
	430 440 450 460 470 480
m134 . pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134 . seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCAG GTAAAACAC  GTTGACTGAA AAACCTTGC
101 TGTTCAGG  TGCATTCAA  AGCGCGGTA  CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTATAAGAC  CACACCGTCA
251 ACCTTTGGA  CACGCCGGA  CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTGACCG CCGTCGATAG TGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCAATA
401 CGCCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAATTGC TGGACGAAGT GGAAAACATC CTGCAAAATC GCTGCGCGCC
501 CGTAACCTGG CCGATCGGCA TGGGCAAAAA CTTCAAAGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCTTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCCGAAT TGGAAACAACG
651 CTTTCCGTTA GAAATACAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTCAAT CTCGACGAAT TCCTCGCCGG CGAATCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGAATGGG CGCCCGCGCC GAAACCACGC GATGCGACCG
851 TGCGTATGGT CGAGCCGAC  GAGCCGAAGT TTTCCGGATT TATCTTCAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG

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951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTG TTCGCGCCCG AACTGTTCCG CAGCGTTCGC
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAAGT GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIGKID NPELEQRFPL EIQLLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDNASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

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m134/a134 98.9% identity in 531 aa overlap

```

m134.pep      10      20      30      40      50      60
MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
|||||:
a134          10      20      30      40      50      60
MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD

m134.pep      70      80      90      100     110     120
IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA
|||||:
a134          70      80      90      100     110     120
IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA

m134.pep     130     140     150     160     170     180
QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPPIGMGKNFKG
|||||:
a134         130     140     150     160     170     180
QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILQIRCAPVTWPPIGMGKNFKG

m134.pep     190     200     210     220     230     240
VYHILNDEIYLFEGGERLPHEFDIIGKIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
|||||:
a134         190     200     210     220     230     240
VYHILNDEIYLFEGGERLPHEFDIIGKIDNPELEQRFPLEIQQLRDEIELVQAASNEFN

m134.pep     250     260     270     280     290     300
LDEFLAGELTPVFFGSAINNFGEIQLNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
|||||:
a134         250     260     270     280     290     300
LDEFLAGELTPVFFGSAINNFGEIQLNSLIEWAPAPKPRDATVRMVEPDEPKFSGFIFK

m134.pep     310     320     330     340     350     360
IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSSVVTFMSHDRELVEEAYAG
|||||:
a134         310     320     330     340     350     360
IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSSVVTFMSHDRELVEEAYAG

```

382

	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGVFAVFDASISWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGVFAVFDNASISWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGAcgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACG GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcGaaa gcggGGgcag cgttTAtgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1  MKYKRIVFKV GTSSITRSDG SLSRGIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVQGG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEI IEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDS LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

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383

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501 GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCAGTG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACG GCGGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CTGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTCATC
1051 CATCGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
1  MKYKRIVFKV GTSSITHSDG SLRSGKIQTI TCQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KOASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRVAP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHINHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGSVYV DEGAEHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

m135/g135

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
g135	MKYKRIVFKVGTSSITRSDGSLRSGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
g135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m135.pep	SVLLQRRVAPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
g135	SVLLQRRAPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m135.pep	NPDAVR LDKI EHINHEIEMAGGSGSANGTGGMLTKIKAATIAAESGVPVYICSSLKPDA					
g135	NPDAVR LDKI EHINHEIEMAGGSGSANGTGGMLTKIKAATIAAESGVPVYICSSLKPD S					
	190	200	210	220	230	240
	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSES RG SVYVDEGA EH ALSEQGKSLLMSGI					
g135	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSES GG SVYVDESA EH ALSEQGKACX					
	250	260	270	280	290	
	310	320	330	340	350	360

384

m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```

a135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TCGCTGCGG TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGTTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGTCTGT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTTCGGC AAACGGCACA GCGGGTATGC TGACTAAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 LCTGGCGTTC TATTCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAGG GCGAGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTGCGTA AGCGGAAAGG CGTGTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```

a135.pep
1  MKYKRIVFKV GTSSITHSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIIEIEM
201 AGGSGSANGT GGMLTKIKAA TIATESGVPV YICSSLKPDA LAEAAADNQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGGVYV DEGAEHALSE QGKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

m135/a135 98.4% identity in 369 aa overlap

```

m135.pep      10      20      30      40      50      60
MKYKRIVFKVGTSSITHSDGSLRSGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG
|||||
a135          10      20      30      40      50      60
MKYKRIVFKVGTSSITHSDGSLRSGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG

m135.pep      70      80      90     100     110     120
FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQIILSRADFADKRRYQNAGGAL
|||||
a135          70      80      90     100     110     120
FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQIILSRADFADKRRYQNAGGAL

m135.pep     130     140     150     160     170     180
SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTNPNPNS
|||||
a135         130     140     150     160     170     180
SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTNPNPNS

m135.pep     190     200     210     220     230     240
NPDAVRLDKIEHNHEIIEIEMAGGSGSANGTGGMLTKIKAATIAAESGVPVYICSSLKPDA
|||||
a135         190     200     210     220     230     240
NPDAVRLDKIEHNHEIIEIEMAGGSGSANGTGGMLTKIKAATIAATESGVPVYICSSLKPDA

```

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	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSES	SRGSVYVDEGA	EHALSEQ	GKSLMSGI		
	::					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSES	SRGGVYVDEGA	EHALSEQ	GKSLMSGI		
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLF	GSAAAEDLLKSRKAKGVFIHRDDWISITP				
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLF	GSAAAEDLLKLRKAKGVFIHRDDWISITP				
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

```

g136.seq
1  ATGGAAATCC GGTTCAGAC AGCATTTTTA CGTTTGGTTC AGatgaAAAC
51  AACGCTtca aTTCtaccg caACACGCCT TGTATTTCCT GccgCTGCCG
101 CACGGACAGG GATCGTTCCT GCCGgtTTTT TCCCCTTCCC TCGGACGGT
151 TTGCGGTTTG TTGATGACCG CCTGCCAGTA GCGGTAGATG Tctgccagcg
201 cgTAAGGCag tTCGGAcgca agttccgccca gctcgccttc ggTGAATTGC
251 AGgcgataa cgccgtttTC CTCTTCGTcG taaatgccgc ccactgccat
301 cacgGGGTAA AACAGCTCTT CAAACGCTTC ATCATCGGCG GCTTCAAACC
351 AATCGGTCGG CACAATGTCC AAACCGTAAA GATAGGCGTT GCACCAAGTG
401 TAAAAATCGC TGCCGCCCTC GCCGTCTCG TAGAGCCACA AATCGGGCAG
451 CTTTTTATCC GACATCGCGG CGGTTGTTTC CATCGCCATT GCCAAAACCA
501 GCCGTTCGAT TTCGGAACGT TCGGCGGCGG TAAATTGCGA TTCGTGCCCC
551 AACACTTCGG GCAGCCAGTC GAGCGGTGCC AATTTGTCCG GCGCGCTCAA
601 CAGCGCCGTC ATAAACCTT GAACCTCGTC GCAACGCATC GTGTTGCCTT
651 GTTCGCTTTT GGCATCCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

```

g136.pep
1  MEIRFQTAFI RLVQMKTNAS ILTATRLVFP AAAARTGIVP AGFFPFPADG
51  LRFVDDRLPV AVDVCQVRVQ FGRKFRQLAF GELQADNAV F LFVUNAHHCH
101 HGVKQLFKRF IIGGFKPIGR HNVQTVKIGV APSVKIAAAL AVVVVEPQIGQ
151 LFIHRGGCF HRHCQNQPF D FGTFGGGKLR FVAQHFGQPV ERCQFVRPAQ
201 QRRHKTLLNV ATHRVALFAF GIQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

```

m136.seq
1  ATGGAAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
51  CGCTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTTTC GCCTTCCCTG
101 CGGACGGTTT GCGGTTTGTT GATGACTGCC TGCCAGTAGC GGTAGATATC
151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG
201 TGAATTGCAG ACGGATAGCG CCGTTTTCTT CTTCGTGCGT AATACCGCCC
251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTCG
351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTATA CAGCCACAAA
401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTTCCA TCGCCATTGC
451 CAAAACCAGC CGTTCGATT TCGGAACGTT GCGGCGGTA AATTGCGATT
501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
551 CCGCTCAACA GCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
601 GTTGCCCTTG TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCCTTTT CAAATGGGTT
701 TTGCGCCCTA TTATCGCCGC AATGCCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

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m136.pep
 1 METNASILTA TRLVFSAAAA RTGIVPACFF AFPADGLRFV DDCLPVAVDI
 51 RQCIRQLGFQ FRQLAFCELO TDSAVFLFVV NTAQCHDGIK QLFKRFIIDG
 101 FKPIGRHNIQ TVKISIAPCV KIAAAVFVFI QPQIGQFFIR HRGGCFHRHC
 151 QNQPFDFGTF GGGKLRFVAQ HFGQPVERCQ FVRPAQQRH KTLNLVATHR
 201 VALFAFGIQQ FAQPPFGCFG KFSGIHHFPF QMGFAPYYRR NAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

m136.pep	10	20	30	40
	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV			
g136	10	20	30	40
	MEIRFQTAFRLRLVQMKTNASILTATRLVFPAAAARTGIVPAGFFPPADGLRFVDDRLPV			
m136.pep	50	60	70	80
	AVDIRQCIRQLGFQFRQLAFCELO TDSAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR			
g136	50	60	70	80
	AVDVCQVRVQFGRKFRQLAFGELQADNAVFLFVVNAAHCHHGKQLFKRFIIGGFKPIGR			
m136.pep	110	120	130	140
	HNIQTVKISIAPCVKIAAAVFVFIQPPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
g136	110	120	130	140
	HNVQTVKIGVAPSVKIAAALAVVVEPQIGQLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
m136.pep	170	180	190	200
	FVAQHFGQPVERCQFVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH			
g136	170	180	190	200
	FVAQHFGQPVERCQFVRPAQQRHKTNLNLVATHRVALFAFGIQQ			
m136.pep	230	240		
	HFPPQMGFAPYYRRNAVX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

a136.seq
 1 ATGGAAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
 51 CGCTGCCGCA CGGACAGGGA TCGTTCCCTGC CTGTTTTCCTG GCCTTCCTTG
 101 CGGACGGTTT GCGGCTTGTT GATGACCGCC TGCCAGTAGC GGTAGATATC
 151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG
 201 TGAATTGCAG ACGGATAGTG CCGTTGTCTT CTTCGTCGTA AATACCGCCC
 251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
 301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC
 351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTCATA CAGCCACAAA
 401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTCCTA TCGCCATTGC
 451 CAAAACCAGC CGTTCGATTT CGGAACGTC GCGCGCGTA AATTGCGATT
 501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
 551 CCGCTCAACA GCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
 601 GTTGCCCTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
 651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCCTTTT CCAATGGGTT
 701 TTGCGCCCTA TTATAGTGGA TTAAATTTAA ATCAGGACAA GGCGACGAAG
 751 CCGCAGACAG TACAAATAGT ACGGCAAGGC GAGGCAACGC CGTACTGGTT
 801 TAAATTTAAT CCACTATATC GCCGCAATGC CGTCTGA

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

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```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVEI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPP  PMGFAPYYSG  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

	10	20	30	40	50	60
m136.pep	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ					
a136	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLLPVAVDIRQCIRQLGFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m136.pep	FRQLAFCELOTDASAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV					
a136	FRQLAFCELOTDASAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m136.pep	KIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLRFVAQHFGQPVERCQ					
a136	KIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLRFVAQHFGQPVERCQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m136.pep	FVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPPMGFAPYYRR					
a136	FVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPPMGFAPYYSG					
	190	200	210	220	230	240
m136.pep	NAVX					
a136	LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC  ATCACcaaTT  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCCGC  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTTA
101 CCTTTCTCGG  CAGAAGGCGC  ATCGCGCAAG  GCTTGTCCGT  TTTTACCAAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGG  GTGTAGTTAT  TGCCATATGG  TTGTTCAGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAAGTGA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATTACCG  ACATTAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCGCA
501 TTACGAAGAT  GCCGAAGCCG  CCGCGCACAA  TCCGCTTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCCGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCGCTT  TATTGCCGAA  TTTGCCGCGC  AACCCGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGGTTGAGCG  TCCCGATGAT
801 TGTTTTGGGT  ATCGTCGGCT  TTGTCCGGTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

```

1  MIIHHQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEggMSFHG
101 GFLGVVIAIW LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNfINGELWG
151 RITDINAFWA MGFPQAHYED AEAAAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSKKPRP TGQTAALFLG GYGVFRFIAE FARQPDDYLG
251 LTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 531>:

```

m137.seq
1  ATGATTACCC ATCCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTCTCGG CAGAAGCGC ATCGCGCAAG GCTTGTCCTT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTTTG GTGTAGTTAT TGCCATACGG TTGTTCGGCC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAT GCCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTACCGTTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTCCTCGGC GGCTACGGCA
701 TATTCGCTT CATTGCCGAA TTCGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 532; ORF 137>:

```

m137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEggMSFHG
101 GFLGVVIAIR LfGRKHGIGF LKLMDTVAPL VPLGLASGRI GNfINGELWG
151 RVTDINAFWA MGFPQARYED AEAAAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGI FRFIAE FARQPDDYLG
251 LTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

m137/g137

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
g137	MIIHHQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
	10	20	30	40	50	60
m137.pep	ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFGRKHGIGF					
g137	ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFSRKHGIGF					
	70	80	90	100	110	120
m137.pep	LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW					
g137	LKLMDTVAPLVPLGLASGRIGNFINGELWGRITDINAFWAMGFPQAHYEDAEAAAHNPLW					
	130	140	150	160	170	180
m137.pep	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					
g137	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					
	190	200	210	220	230	240
m137.pep	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					
g137	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					

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```

g137      |||||:|:|||||:|:|||||:|:|||||
          AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKPRPTGQTAALFLGGYGVFRFIAE
          190      200      210      220      230      240

          250      260      270      280
m137.pep  FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX
          |||||:|:|||||:|:|||||:|:|||||
g137      FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 533>:

```

a137.seq
1  ATGATTACCC ATCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCGCC TGGTATGCC TAAGCTACAT CCTCGGATT ATTCTTTTTA
101 CCTTCTCGG CAGAAGCGC ATCGCGCAAG GCTTGTCCGT TTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGCG ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTCCACGGC
301 GGCTTTTTTG GTGTAGTTAT TGCCATATGG TTGTTCCGTC GCAAACACGG
351 CATCGGCTTC CTCAAACCTGA TGGACACGGT CGCACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCC TTTGCGCGTC GTTTGGCTGT TCTCTAAAAA
651 ACAGCGGCCG ACCGGACAAG TCGCCTCACT CTTCCTCGGC GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTTGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 534; ORF 137.a>:

```

a137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEKGMSFHH
101 GFLGVVIAIW LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RVTDINAFWA MGFPQARYED LEAAAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSSKKQRP TGQVASLFLG GYGIFRFIAE FARQPDDYL
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

m137/a137 98.2% identity in 283 aa overlap

```

m137.pep      10      20      30      40      50      60
MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
|||||
a137           10      20      30      40      50      60
MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
|||||

m137.pep      70      80      90      100     110     120
ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFGRKHGIGF
|||||
a137           70      80      90      100     110     120
ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFGRKHGIGF
|||||

m137.pep     130      140      150      160      170      180
LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW
|||||
a137         130      140      150      160      170      180
LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDLEAAAHNPLW
|||||

m137.pep     190      200      210      220      230      240
AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLFSSKKQORSTGQVASLFLGGYGIFRFIAE
|||||:|:|||||:|:|||||:|:|||||
a137         190      200      210      220      230      240
AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKQORPTGQVASLFLGGYGIFRFIAE
|||||:|:|||||:|:|||||:|:|||||

```

390

	190	200	210	220	230	240
	250	260	270	280		
m137.pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQH	X				
a137	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQH	X				
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

g138.seq

```

1  ATGGAGTTTG AAAACATTAT TTCCGCCGCGc gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACAtcc gccgGTTTTC CGGTTCCGTC GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGCG ATTCAATCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGA AAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAGAGAGC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGGTCGATG ATTTTAGGCA GAGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

g138.pep

```

1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAQVM DKTGNLLTKL TPKRIDGLIA DGTLYGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

m138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGGTTTTC CGGTTCCGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGCG ATTCAATCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGA AAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAGAGGCG GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTTTCGATG ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

m138.pep

```

1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```

391

```

51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGGGEDA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 138 shows 98.0% identity over a 298 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m138/g138

	10	20	30	40	50	60
m138.pep	MESENII SAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
g138	MEFENII SAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKV GKKGEFVQGM RVTDKAMDI VEMVLGGHVNKEIVSMINTY					
g138	IHPVIVHGGGPQINAMLEKV GKKGEFVQGM RVTDKETMDI VEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
g138	GGHAVGVSGRDDHFIKAKKLLVDTPEQNSVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKL LMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
g138	VGVGEKGEAFNINADLVAGKLAELNAEKL LMMTNIAGVMDKTGNLLTKLTPKRIDGLIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
g138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGRGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

a138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CTTTACATCC GCCGTTTTC CGGTTCGGTC GCCGTCATCA
101 AATACGCGCG CAACGCGATG ACCGAACCTG CTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCC GTGCGGCTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CCGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACG ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGCGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGGTGC CCAACGCGCT TTTGCTGGA ATCTTTACCG
851 ATGCCGGTAT CGGTTCGATG ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
 51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
101  VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151  DIGQVGTVES IDTGLVKGLI ERGCIPVAP VGVGEKGEAF NINADLVAGK
201  LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251  KIASAVEAAV NGVKATHIID GRVNPALLLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
a138	MESENIISAAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAEEELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAEEELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVNPALLLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
 51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAggc ggcggcggag
101  gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151  AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201  AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCCGGATG
251  ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301  ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351  CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401  GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAACTG
451  TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAATTACA
501  AAAACTATAC GCGGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
 51  NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101  IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
151  YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
  1 ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGACTGCCAT
 51 GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGTACCGG TATCGGCAGC
151 AACAGCAGAG CAACAACAGC GAAATCAGCA GCAGTATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCTGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTCCA AACCCTAAATG ACGCATtACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTACG AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.pep
  1 MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
 51 NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETFQTM THYKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE
151 LYGRKEHGYN ENYEKLYGVY AEGSA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

```
m139/g139

      10      20      30      40      50      60
m139.pep MRTTPTFPTKTFKPTAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
g139      MRTTSTFPTKTFKPAAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATIAESA
      10      20      30      40      50      60

      70      80      90     100     110     120
m139.pep AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFQTMTHYKNLINLK
g139      AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIKAP-RICIPETFQTMINIKNMINLK
      70      80      90     100     110

      130     140     150     160     170
m139.pep PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX
g139      PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX
      120     130     140     150     160     170
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

```
a139.seq
  1 ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
 51 GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACAACAGC GAAATCAGCA GCAATATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCTGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTACA AACCCTAAATG ACGCAT. ACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTAC. AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

```
a139.pep
  1 MRTTPTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
```

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51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
 101 CIPETLQTOM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ES VGSI SFPE
 151 LYGRKEHGYN ENYXKLYGVY AEGSA*

m139/a139 97.1% identity in 175 aa overlap

	10	20	30	40	50	60
m139.pep	MRTTPTFPKTFKPTAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA	
a139	MRTTPTFPKTFKPAAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGR	DDVAVTDRDAKINAPPRICIPET	FQTMTHYKNLINLK			
a139	AISYAGIKNEMCKDRSMLCAGR	DDVAVTDRDAKINAPPRICIPET	LQTOMTHXKNLINLK			
	70	80	90	100	110	120
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPELYGRKEHGYN	ENYXKLYGVYAEGSAX			
a139	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPELYGRKEHGYN	ENYXKLYGVYAEGSAX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

g140.seq

1	Atgtcggcac	gCGGCAAGGG	GGCAGgctat	ctcAACAGTA	CCGGACGACa
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	AAAATATCAA	AACCGACGGC	GGTCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCAGTGAAGG	CGACACGCCG	TCCTATTATG	TCCGTCGCGG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACATTCCGCG	CCCGCCGGTC
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGA AAA	CCTGATGGTC
301	GAGCTGGATG	CCTCCGAATC	ATCCGCAACA	CCCAGACCGG	TTGAAACTGC
351	GGTCGCCGAC	CGCACAGATA	TGCCGGGCAT	CCGCCTACGG	CGCACA ACTT
401	TCCGCACAGC	GGCAGCCGTA	CAGCATGCGA	ATACCGCCGA	CGCGGTACGc
451	aTCTTcaaCA	GTCTCGCCGC	TAccgTCTAt	GccgACAGTG	CCGCCGCCCA
501	TGccgATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTTGGACC
551	ACAACGGTAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGGCGGTGT	CGAAGGCAAA	ATGCGCGGCA	GTACCCAAAC
651	TATCGGCATT	GCCGCGAAAA	CCGGCGAAAA	TACGACAGCA	GCCGCCACAC
701	TGGGCATAGG	ACGCAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAACC
751	GACAGCATTa	GTCTGTTTGC	AGGCATACGG	CACGATGTGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTTCT	CctaCGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACC GG	TGCGGATGAA	TATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	TGGTGTCAAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTTGACG	GTTGAAGGCG	GTCGCGCCA	CGACCTGCTC	AAACAGGATG
1001	CATTTCGCCG	AAAAGGCagt	GCTTTGGGCT	GGAGCGGCAA	CAGCCTCACT
1051	GAAGGCACAC	TGGTCGGACT	CGCGGGTCTG	AAACTGTTCG	AACCCTTGAG
1101	CGATAAAGCC	GTCTGTCTTG	CGACGGCGGG	CGTGAACGC	GACCTGAACG
1151	GACGCGACTA	CGCGGTAACG	GGCGGCTTTA	CCGGCGCGGC	TGCAGCAACC
1201	GGCAAGACGG	GTGCACGCAA	TATGCCGCAC	ACCCGCCGGG	TTGCCGTCTT
1251	GGGGGTGGAT	GTCGAATTCT	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACACCGG	TTCCAAACAG	TACGGCAACC	ACAGCGGACA	AATCGGCGTA
1351	GGCTACCGGT	TCTGA			

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

g140.pep

1	MSARGKGAGY	LNSTGRHVPF	LSAAKIGQDY	SFFKNIKTDG	GLLASLDSVE
51	KTAGSEGDTP	SYVVRRGNAA	RTASAAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESSAT	PETVETAVAD	RTDMPGIRLR	RTTFR TAAAV	QHANTADGVR
151	IFNSLAATVY	ADSAAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQQDGG
201	TWEQGGVEGK	MKGSTQTIGI	AAKTGENTTA	AATLGIGRST	WSENSANAKT

395

```

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRHDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAAT
401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV
451 GYRF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

```

m140.seq
1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG
51 TGTTCCTTC CTGAGTGCCG CCAAAATCGG GCAGGATTAT TCTTTCTTCA
101 CAAACATCGA AACCGACGGC GGCCTGTCTG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GCACTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCGCGC CCGCCCGGTC
251 TGAAACACGC CGTAGAACAG GGCAGGAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCGGAGACGG TTGAAACTGC
351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GGCACCACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTA GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG
951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
1051 GAAGGCACGC TGGTCGGACT CGCGGGTCTG AAGCTGTGCG AACCTTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAAACG GACCTGAACG
1151 GACGCGACTA CACGGAACG GCGGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

```

m140.pep
1 MSARGKGAGY LNSTGRRVPF LSAAKIGQDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDITL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNSLAATVY ADSTAADADM QGRRRLKAVSD GLDHNGTGRLR VIAQTQDQGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

```

m140/g140
10 20 30 40 50 60
m140.pep MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g140 MSARGKGAGYLNSTGRHVPFLSAAKIGQDYSFFKNIKTDGGLLASLDSVEKTAGSEGDTP
10 20 30 40 50 60
70 80 90 100 110 120

```

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m140.pep	SYVVRGNAARTASAAAH SAPAGLK HAVEQGGSNLENLMVELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAH SAPAGLK HAVEQGGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140.pep	130 140 150 160 170 180
	RTDMPGIRPYGATFRAAAVQHANAADGVRI FNSLAATVYADSTAAHADMQGRRLKAVSD
g140	RTDMPGIRLRRTTFR TAAVQHANTADGVRI FNSLAATVYADSAAAHADMQGRRLKAVSD
	130 140 150 160 170 180
m140.pep	190 200 210 220 230 240
	GLDHNGTGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQDDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLGIGRST
	190 200 210 220 230 240
m140.pep	250 260 270 280 290 300
	WSENSANAKTDSISL FAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISL FAGIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140.pep	310 320 330 340 350 360
	MQLGALGGVNPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
g140	MQLGALGGVNPFAATGDLTVEGGLRHDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
	310 320 330 340 350 360
m140.pep	370 380 390 400 410 420
	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVAGLGVD
	370 380 390 400 410 420
m140.pep	430 440 450
	VEFGNGWNLARYSYAGSKQYGNHSGRVGVG YRFX
g140	VEFGNGWNLARYSYTGSQYGNHSGQIGVG YRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140.seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCTTC CTGAGTGCCG CCAAAATCGG GCGGGATTAT TCTTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTGCGGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCGCCCGGTC
251 TGAACACAGC CGTAGAACAG GGCGGCAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGCGCAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG

```

```

951 AGATTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGCTGG TTGCCGGTCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

```

a140.pep
1 MSAGGKGAGY LNRTGQRVFP LSAAKIGRDY SFFTNIETDG GLLASLDSVE
51 KTAGSEDTL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRLKAVSD GLDHNATGLR VIAQTQDGG
201 TWEQGVVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLG GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

```

m140.pep      10      20      30      40      50      60
MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEDTL
||| ||||| ||:|||||||:|||||||
a140          10      20      30      40      50      60
MSAGGKGAGYLNRTGQRVFPFLSAAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEDTL

m140.pep      70      80      90      100     110     120
SYVRRGNAAARTASAAHSAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD
|||||:|||||:|||||:|||||:|||||:|||||
a140          70      80      90      100     110     120
SYVRRGNAAARTASAAHSAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD

m140.pep     130     140     150     160     170     180
RTDMPGIRPYGATFRAAAVQHANAADGVRIFNSLAATVYADSTAAHADMQGRRLKAVSD
|||||:|||||:|||||:|||||:|||||:|||||
a140         130     140     150     160     170     180
RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLAATVYADSTAAHADMQGRRLKAVSD

m140.pep     190     200     210     220     230     240
GLDHNATGLRVIAQTQDGGTWEQGVVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
|||||:|||||:|||||:|||||:|||||:|||||
a140         190     200     210     220     230     240
GLDHNATGLRVIAQTQDGGTWEQGVVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST

m140.pep     250     260     270     280     290     300
WSENSANAKTDSISLFAGIRHDAGDIGYLGKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
|||||:|||||:|||||:|||||:|||||:|||||
a140         250     260     270     280     290     300
WSENSANAKTDSISLFAGIRHDAGDIGYLGKGLFSYGRYKNSISRSTGADEHAEGSVNGTL

m140.pep     310     320     330     340     350     360
MQLGALGGVNVFPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
|||||:|||||:|||||:|||||:|||||:|||||
a140         310     320     330     340     350     360
MQLGALGGVNVFPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL

m140.pep     370     380     390     400     410     420
KLSQPLSDKAVLFFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
|||||:|||||:|||||:|||||:|||||:|||||
a140         370     380     390     400     410     420
KLSQPLSDKAVLFFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD

```

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	370	380	390	400	410	420
	430	440	450			
m140.pep	VEFGNGWNGGLARYSYAGSKQYGNHSGRVGVGYRFX					
a140	VEFGNGWNGGLARYSYAGSKQYGNHSGRVGVGYRFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAAccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGCGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTC GCGTGAAGG CGGCGCGGCA GCGCGCGGCT ACGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGCGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTtga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTGa tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTtTt gGCAATATTC TCGTCGCGTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCTT GACCGAAGTG TGGGGCAAAG GCGGCGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACSTCGG TTTTCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTCG ATTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCCGGC GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCTT GCCGAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pep

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGA GGGYAQVLPM EDINLHFTGD PHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKVPDVGM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVVNAID NQPNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEKIDVDE
551 HGVIHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGCGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TGC GCGAACC TTCTCTGGGG
301 CCGGTGTTTC GCGTGAAAGG CGGCGCGGCA GGCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GGCGGCGCGT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCGGTTGA CGGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCGCGCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAATGCGCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGA AAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACGC CGATGCCGAG TTGGCGATGA TTGAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAGT GTACGGCGCG GAAGATGTTG ATTTAGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCCT
1551 TTCCGACGGC GCAGGTTTCA TCGTCGCCCT GTGCGCAAC ATGATGAAAA
1601 TGCCCGGCTT GCCCAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHIKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFGVKGGAA GGGYAOVLPD EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPVGDVM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAI AQKVYGA EDVDFSABAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

	10	20	30	40	50	60
m141.pep	MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHIKAKINPAEAFKL					
g141	MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHIKAKINPAEAFKL					
	10	20	30	40	50	60

400

m141.pep	70	80	90	100	110	120
	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLP					
g141	70	80	90	100	110	120
	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLP					
m141.pep	130	140	150	160	170	180
	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVVDMDRQLRNIID					
g141	130	140	150	160	170	180
	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVVDMDRQLRNIID					
m141.pep	190	200	210	220	230	240
	GMGKPVGDGVMRPDGFDTVASEVMAVFCIAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
g141	190	200	210	220	230	240
	GMGKPVGDGVMRPDGFDTVASEVMAVFCIAKDISDLKERFGNILVAYAKDGSPVYAKDLK					
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIETPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
g141	250	260	270	280	290	300
	AHGAMAALLKDAIKPNLVQTIETPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
m141.pep	310	320	330	340	350	360
	GFGADLGAKEFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	310	320	330	340	350	360
	GFGADLGAKEFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
m141.pep	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVESLTEVWGKGGAGGAD					
g141	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDSDAELAMIEKACAEHGVESLTEVWGKGGAGGAD					
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
g141	430	440	450	460	470	480
	LARKVVNAIDNQPNNGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

```

a141.seq
1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAAC TG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

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201 GCGGGGCGAA GGTAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGGCGGGCT ATGCCCCAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTTCG CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCAGAGCA
901 GGCTTCGGCG CGGACTTGCG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTGCCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCCGAC TGCCCGTCGT CGTTGCGCTC AACCCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACTTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPV DGVM RPDGFITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGEVSLTEV WKGAGGAGD LARKVVNAIE SQTNNFGFAY DVELGKDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

m141.pep      10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL
|||||:|||||
a141          10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL
|||||:|||||

m141.pep      70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFVGKGAAGGGYAQVLPM
|||||:|||||
a141          70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFVGKGAAGGGYAQVLPM
|||||:|||||

m141.pep     130     140     150     160     170     180
EDINLHFTGDFHAI GAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
|||||:|||||
a141         130     140     150     160     170     180
EDINLHFTGDFHAI GAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
|||||:|||||

```

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	190	200	210	220	230	240
m141.pep	GMGKPV DGV MRPDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
a141	GMGKPV DGV MRPDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGA EKFC DIKCR LAGLKPDA AVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGA EKFC DIKCR LAGLKPDA AVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVESLTVWVGKGGAGGAD					
a141	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVESLTVWVGKGGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRATAQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRATAQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1   ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
151 GGCAACATCC TGATGTTTCGT CCGCCAGCAT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATcggaATG AttcgCGCAC TCCGTTTAT GCACAGCATC
251 ACGGTCGGCG GTCGTCGGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC CGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1   MRADFMFADN MPVQVRQRAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMF
51  GNILMFVRQH IDAEAAVFRQ DRNDSRTPVY AQHHGRRLVG NRRNRRCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLSKF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQQF*

```


The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
 51 ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCcC ATGTGCAGCA GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
  1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTVPD AQHHGRRLLV NRRDRRHCHNA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQQF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142

      10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFGNILMFVRQR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVGKPLFGRQAGQPGKMFGNILMFVRQH
          10      20      30      40      50      60

      70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTVPDAQHHGRRLLVGNRRDRRHCHNAVTPCRTVCRDDMNACRARCH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g142      IDAEAAVFRQDRNDSRTVPVYAQHHGRRLLVGNRRRRRHCHNAVTPCRTVCRDDMNACRTGCH
          70      80      90      100     110     120

      130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g142      RITERSLKSFQIRHFSPLNRPLYKNAAHKASPHVQQFX
          130     140     150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
 51 ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCCGACAT
501 TTCCGCGCGT TACGGCGTAT TACGAGTTCA ACGCATCCTC GATTTTGCCA
551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGCCAGCAC
601 TTCCTCGATA GCGTCGTAAC GCTCGTCCAC TTCTTCGCCG ATTTCCTCAT
651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAAACACG TCGTTGGTGC
701 TTGGAAGGTT TCAGGCGGAC AACCAAACCC GCTTTTCAA GGCGGGTCAG
751 GATACCGGTC AGGCTGGGGC GCAAAATGCA CGCCTGATTG GCCAAATCTT
```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLLVR NRRNRRHCNA
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK
 151 APPMCSSSDS KSRRSDISAR YGVLRVQRIL DFGKFCQQVF KQOHFLAAQH
 201 FLDSVVTLVH FFADFLIQLL ALGSQLOKNT SLVVGRFQAD NQTRFFKAGQ
 251 DTGQAGAQNA RLIRQILKVQ RAVFRQKTDN PPLLIGNIRL IQNRPFLGHQ
 301 GFPCLYQTDI DRRMF*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNGNILMFVRQR					
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNGNILMFVRQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVNRNRRRHCAVTPCRTVCRDDMNACRTGCH					
	70	80	90	100	110	120
	130	140	150	159		
m142.pep	RITERSLKI FLQIRHFSPLNCPLYKNAAHKASPHVQQFX					
a142	RITERSLKSFLQIRHFSPLNCPLYKNAAHKAPPMCSSSDSKSRRSDISARYGVLRVQRIL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a142	DFGKFCQQVFKQOHFLAAQHFLDSVVTLVHFFADFLIQLLALGSQLOKNTSLVVGRFQAD					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAAG
 51 CTCGCAGATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAATT
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTCAGCCG
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCCTGGCG
 301 GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGATATG GTCACGAGG
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAA GTTCTTAGC GAATACGGAC
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCCTGGTC GTAGCATTCT
 551 ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTCAC AATCTCCAAA
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC
 701 CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTCTCTC CTGGTTCGCC
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGCTCTG
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT
 851 ACGGCGTTTT GGCGCGGGTG TAGTCGGTTG CGGCGGTGAT TTGTTCTGTTT
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGGCGGGTT ATTTCCGGCTG
 951 TTTGGCTTTG GGCGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC
 1001 AATACGCACT CATCCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTTGT CGGGCAAAACA
 1101 CATGGATACT TATTGGGGCC TGTttaacgg ctctgtCTGT ATGCcgcaaa
 1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

405

1201 CAGGCAACCA TGTTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep
 1 MLSFYGLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGYSDRTW KPRLGGRRLP YLLYGTLLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKSYAY GIQSFLANTD
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFMTV TPVQFFCWFA
 251 FRYMWYSAG AIAENVWHTT DASSVGHQEA GNRYGVLAHV *SVAVICSF
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNQYALILS YILIGIAWAG
 351 IITYPLTIVA NALSGKHMMDT YLGLFNFSVC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq
 1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTCACTCCTG CCGCCGCTGG CGGGGATGCT GGTGCAGCCG
 151 ATTGTGCGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
 201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTTCTTAGC AAATACGGGC
 451 GCGTCTGTGG CGGCGATTCT GCCGTTTGTG TTTGCGTATA TCGGTTTGGC
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT
 551 ATGTGGGTGC GCGTGTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC
 701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTTCGCC
 751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
 801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT
 851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CGGCGGTGAT TTGTTCTGTT
 901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTTCGGCTG
 951 TTTGGCTTTG GCGCGCTCG GCTTTTTCTC CGTTTTCTTC ATCGGCAACC
 1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
 1101 TATGGGCACT TACTTGGGCT TGTTTAAACGG CTCTATCTGT ATGCCTCAAA
 1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
 1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
 1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep
 1 MLSFYGLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGHYSDRTW KPRLGGRRLP YLLYGTLLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGYAY GIQSFLANTG
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFMTV TLVQFFCWFA
 251 FQYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAHV QSVAVICSF
 301 VLAQVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
 351 IITYPLTIVT NALSGKHMDT YLGLFNFSIC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVGGV VLLLGAFSVC LIKETHGGV*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

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al43.seq
1  ATGCTCAGTT  TCGGCTTTCT  CGGC GTTCAG  ACGGCCTTTA  CCTGCAAAG
51  CTCGCAGATG  AGCCGCATCT  TCCAGACGCT  CGGTGCCGAT  CCGCACAGCC
101 TCGGCTGGTT  CTTTATCTCG  CCGCCGCTGG  CGGGGATGCT  GGTGCAGCCG
151 ATTGTCGGCC  ATTACTCCGA  CCGCACTTGG  AAGCCGCGTT  TGGGCGGCCG
201 CCGTCTGCCG  TATCTGCTTT  ATGGCACGCT  GATTGCGGTT  ATTGTGATGA
251 TTTTGTATGCC  GAACTCGGGC  AGCTTCGGTT  TCGGTTATGC  TGTGCTGGCG
301 GCTTTGTGCT  TCGGCGCGCT  GATGATTGCG  CTGTTAGACG  GTCGTCAAA
351 TATGGCGATG  CAGCCGTTTA  AGATGATGGT  CGGCGACATG  GTCAACGAGG
401 AGCAAGAAAG  CTACGCCTAC  GGGATTCAAA  GTTTCCTTAG  GAATACGGGC
451 GCGGTCTGTG  CGGCAGTTCT  GCCGTTTGTG  TTTGCGTATA  TCGGTTTGGC
501 GAACACCGCC  GAGAAAGGCG  TTGTGCCGCA  GACCGTGGTC  TGGCGTTTTT
551 ATGTGGGTGC  GGC GTTGCTG  GTGATTACCA  GCGCGTTCAC  GATTTTCAA
601 GTGAAGGAAT  ACAATCCGGA  AACCTACGCG  CGTAACCACG  GCATCGATGT
651 CGCCCGCAAT  CAGGAAAAAG  CCAACTGGAT  CGAATCTTGT  AAAACCGGCG
701 CTAAGGCGTT  TTGGACGGTT  ACTTTGGTGC  AATTCTTCTG  CTGGTTGCGC

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751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGGT
851 ACGGCGTTTT GCGGCGGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCTGTTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCTGGCTG
951 TTTGGCTTTG GCGCGGCTCG GCTTTTTCTC CGTTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTAACGG CTCTATCTGT ATGCCGCAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  MLSFGFLGVQ TAFTLQSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTIV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWTSYAG AIAENVWHTT DASSVGYQEA GNWYGVLAAG QSVAAVICSF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMGLGL
401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

```

          10      20      30      40      50      60
m143.pep  MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
          |||||:|||||
a143      MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHSLGWFFILPPLAGMLVQPIVGHYSDRTW
          10      20      30      40      50      60

          70      80      90     100     110     120
m143.pep  KPRLGGRRLPYLLYGTLIIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
          |||||:|||||
a143      KPRLGGRRLPYLLYGTLIIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
          70      80      90     100     110     120

          130     140     150     160     170     180
m143.pep  QPFKMMVGDMVNEEQKGAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTIVV
          |||||:|||||
a143      QPFKMMVGDMVNEEQKGAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTIVV
          130     140     150     160     170     180

          190     200     210     220     230     240
m143.pep  VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
          |||||:|||||
a143      VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
          190     200     210     220     230     240

          250     260     270     280     290     300
m143.pep  TLVQFFCWFAFQYMWTSYAGAIENVWHTTDASSVGYQEAGNWYGVLAAGQSVAAVICSF
          |||||:|||||
a143      TLVQFFCWFAFQYMWTSYAGAIENVWHTTDASSVGYQEAGNWYGVLAAGQSVAAVICSF
          250     260     270     280     290     300

          310     320     330     340     350     360
m143.pep  VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
          |||||:|||||
a143      VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
          310     320     330     340     350     360

          370     380     390     400     410     420
m143.pep  NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMGLGLQATMFLVGGVVLLLGAFSVF

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```

a143      |||||
          NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVVLLLGAFSVF
          370      380      390      400      410      420

          430
m143.pep  LIKETHGGVX
          |||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATCGGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGGG GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGCAC GGGCTGGCCG TTACCGgtTT
351 CAACGCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTTGGatatt
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGTtaccT ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCGGCCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFVSLADGV
51  RENPVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GR TYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGYFLPLGRG RPYRYLSRH
151 RARRHGVRPD AAHLLAAGRG PARCGSAYS A GRTYSGRCRK TARLNGFRRP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATCGGGACAA
201 TCCGTTTCAG ATTAACAAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGG GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTTCGGT GGTGCTGCGC AGCCGCTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCTTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TA cCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFVSLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GR TYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFEGFYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARCG SAY SAGRTYA
201 GRCRK TARLN GFRRPSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRD FGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD
          |||||||
g144      MSDTPATRD FGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFSVLADGVRENPFVVSFDD
          10      20      30      40      50      60

      70      80      90     100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          |||||||
g144      AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          70      80      90     100     110     120

      130     140     150     160     170     180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFGYFLPLGRGRPAYRYLSRHRARRHGVRPDA AHL
          |||
g144      AAD-----GRRLSQRFG--YFLPLGRGRPAYRYLSRHRARRHGVRPDA AHL
          130     140     150     160

      190     200     210     219
m144.pep  AAGRGPARGSAYSAGRTYAGRCRK TARLNGFRPRSIX
          |||||||
g144      AAGRGPARGSAYSAGRTYSGRCRK TARLNGFRPRSIX
          170     180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

```

a144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTTC GGCCTGATCG ACGGGCGGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCCGAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTCCGT GGTGCTGCGC AGCCGCCTG.
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TACCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATTCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

```

a144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFSVLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GR TYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLXTVGRRL SQRFGFGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDA AHL AAGRGPARGS SAYSAGRTYS
201 GRCRK TARLN GFRRPRSI*

```

m144/a144 99.1% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD
          |||||||
a144      MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD
          10      20      30      40      50      60

      70      80      90     100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV

```

410

```

|||||
a144      AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
              70          80          90          100          110          120

              130          140          150          160          170          180
m144.pep  AADGRSVVLSRLATVGRRLSQRFGFGYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
|||||
a144      AADGRSVVLSRLXTVGRRLSQRFGFGYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
              130          140          150          160          170          180

              190          200          210          219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
|||||
a144      AAGRGPARGCSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
              190          200          210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1   ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51  AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA ctTCCCGACT GTCCGTCCCG CGCctTTGA GGCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCCTCC TGCGCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTATGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGAC ACCCTATTTT
601 ATATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.pep
1   MKQIPLRLLO VVIDHDKVEQ YGLFDFMPCL RQPPLDNFPT VRPAPFEARG
51  KHVERRRQDK DTDSFRQVA NLRRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKRFK LFFGNKVIMY AVCFAFTRRA RMRHGNAT
151 VMVCQQRHQ  RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1   ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51  AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTTGA GGCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCCGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAC CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCCG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTGTGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1   MAQILLRSRQ VVIDHDKVKQ YGLLDFMPCL RQPPLDNFPT VRPASVEARG
51  KYVERRRQDK DADGFGQVA NLRRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSFLRDKRLK LFFGNKVIMY AVCFAFTRRA RVRHGNAT
151 VMVCQQRHQ  RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```


Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
g146	MKQIPLRLLQVVVIDHDKVEQYGLDFMPCLRQPPLDNFPTVRPAPFEARGKHVERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m146.pep	DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK					
g146	DTDSFRQVRVANLRRALNVDFQNHVIACRRQRIHALRACAVIVAEYVCVFQKSLLRDKRKF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m146.pep	LFFGNKVIMYAVCFATRRARRVRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS					
g146	LFFGNKVIMYAVCFATRRARRMRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS					
	130	140	150	160	170	180
	190	200	210			
m146.pep	GHIFYLYIFQPIVSQWTPSFLFADAHILPLLF					
g146	GHIFYLYIFQPIVSQRTPYFIFADAHILPLLF					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```
a146.seq
1   ATGGCGCAAA TCCTCCTCCG CCCGCGCCAA GTCATCATTG ACCACGACAA
51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCTCGACT GTCCGTCCCG CGTCCGTGTA GACGCGCAGC
151 AAGCACATCG AAAGACGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTC CAAAATCAGC
251 TCATAACCTG CCGCCGCCAA CGCATTACAC CCCTCCGCGC TTGTGCCGTA
301 ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TGC GCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGACG CGTCGTGTGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601 CTATTTGCCG ATGCCCATAT TTGCGCGCTA TTGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

```
a146.pep
1   MAQILLRPRQ VIIDHDKIEQ YGLDFMPCL RQPPLDNFPT VRPASVETRS
51  KHIERRRQDK DADGFGQRIS NLSRALNVDF QNHVITCRRQ RIHTLRACAV
101 IVAEHVRVFQ KSLLRDKRLK LFFGNKVIMY AVCFAETRRT RVRHGNAT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPGF
201 LFADAHILPL LF*
```

m146/a146 90.6% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
a146	MAQILLRPRQVIIDHDKIEQYGLDFMPCLRQPPLDNFPTVRPASVETRSKHIERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120

412

```

m146.pep  DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK
          |||||::||| |||||::||| |||||::||| |||||::||| |||||::||| |||||
a146      DADGFGQRI SNLSRALNVDFQNHVITCRRQRIHTLRACAVIVA EHVRFQKSLLRDKRLK
          70      80      90      100     110     120

          130     140     150     160     170     180
m146.pep  LFFGNKVIMYAVCFATRRARRVRHGN AQTVMVCQQPRHQRFARAGSGRNDKDVAFSIS
          |||||::||| |||||::||| |||||::||| |||||::||| |||||::||| |||||
a146      LFFGNKVIMYAVCFATRRARRVRHGN AQTVMVCQQPRHQRFARAGSGRNDKDVAFSIS
          130     140     150     160     170     180

          190     200     210
m146.pep  GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX
          |||||::||| |||||::||| |||||::||| |||||::||| |||||::||| |||||
a146      GHIFYLYIFQPIVSQRTPGFLFADAHILPLLFX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGGCTGCT GCACACTTCG ACCGCCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAAGTAT TGAACCATCA
351 CGGCGAAACG GCGGATATGG CGGACTTTTC TCCCGATCAC GCCATTATGG
401 TAGATACCGC CTTGTCGCAA CAGGTGAAA TCCTGCGCGG GCCGGTTACG
451 CTCTTGTA CA GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc ccaaaaAAtg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLKPIVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHGET GDMADFS PDH AIMVDTALSQ QVEILRGVPT
151 LLYSSGNVAG AGQCCRWNKP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTTG GAAACGGTCA GCGTCGTCGG
51  CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGACACT TCGACCGCCT
101 CCGACAAAAT CATCTCCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GGCGACGCTT TAGACGGCGT ACCGGGCATC CACGCTTCG AATACGGCGG
201 CGGCGCGTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAAG
251 TGTTGAACCA TCACGGCGAA ACAGGCGATA TGGCGGATTT TTCGCCGAT
301 CACGCCATTA TGGTAGATAC CGCCTTGTCG CAACAGGTCG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAAA TGCCTGAAAA CGGCGTATCG
451 GGCGAACTCG GATTGCGTTT GAGCAGCGGC AATCTGAAA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAAA CTTGTATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGCGTTA CCGCAATCTG
601 AAACGCCTGC CCGAGCCA CGCGATTTC CAAACGGGCA CCGCGGCT
651 GTCTTGGGTT GGCGAAAAAG GTTTTATCGG CGTAGCGTAC AGCGACGTC
701 GCGACCAATA TGGTCTGCCT GCCCAGACC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCCACGAC GACGATAATG CACACGCACA CACCCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGCTACGAAC TCCGTGCCGA
951 ATGGAAGCAA CCGTTCCCG GTTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAGCAG GCGATGCAGT CGAAAACCTT
1051 TTAAACAACC AAACGCAAAA CGCCCGCATC GAGTTGCGCC ACCAACCCAT

```

413

```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACACG CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACATACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC CGACTTCTAC GCGCGGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTT GGACTACTAC CGCGTGTTCG CCGGCAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAACCTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCCACA GCAGCTTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGGCGGC GTGAACGTGA
2201 AGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMADFSFD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNFVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTGSIGLSWV GEKGFIGVAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRHD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGRL KGSWGVQYLQ QKSSALS AIS EAVKQPMMLD
401 NKVQHYSFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENNYHNP
451 LPDLGAHRQT ARSFALSGNW YFTPQHKLSL TASHQERLPS TOELYAHGKH
501 VATNTFEVGN KHLNKRSSNN IELALGYEGD RWQYNLALYR NREFGNYIYAQ
551 TLNDGRGPKS IEDDSEMCLV RYNQSGADFY GAEGEIFYFK TPRYRIGVSG
601 DYVRGRGLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

                                10      20      30
m147.pep                      PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
                                |:||||| |
g147      MRREAKMAQITLKP I VLSILLINTPLLAQA HETE QSVGLETVSVVGKSR PRATSGLLHTS
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m147.pep      TASDKIISG DTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
              |||
g147      TASDKIISG DTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
              70      80      90      100     110     120

                                100     110     120     130     140     150
m147.pep      GDMADFS PDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLV D VADGKI PEKMPENGVS G
              |||
g147      GDMADFS PDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCR WKNPPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```
a147.seq
1   ATGCGACGAG AAGCCAAAAT GGCACAAACT AACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCAAGCG CATGGAAGTG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCGG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCAGC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATTTCAT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAGTGT TGAACCATCA
351 CGGCGAAACG GGCACATGG CCGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTGCGAA CAGGTCGAAA TCCTGCGCGG TCCGTTACG
451 CTCTTGACAC GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGCGTTTGAG CAGCGGCAAT CTGGA AAAAC TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACCT TGTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCGAA ACGGGCAGCA TCGGGCTGTC TTGGGTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATAAGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCGCGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTT AACAACTAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTCACGCTT
1351 GAAGGCGGCG TACGCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCATC AGGAACGCCT
1551 GCGTCAACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCCGGCGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCCTC GCGTTCCGGC
2001 TGCGCGCCTC GCGGTCCACC TGAAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTTGGA CTACTACCGC GTGTTGCGCC AAAACAAACT CGCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAAA GCCGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA
```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```
a147.pep
1   MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFS PDH AIMVDSALSQ QVEILRGFVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVS ELGLRLSSGN LEKLTSGGIN
201 IGLKNFVLH TEGLYRKSGD YAVPRYRNLK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEDIDIDYN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNAIE LRHQPIGRK
401 GSWGQYLQK KSSALSATSE AVKQPMLLDN KVQHSFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYNHPL PDLGAHRQTA RSFALSGNWX
501 FTPQHKLST ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR
```

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601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYYR VFAQNKALARY
701 ETRTPGHHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP
751 QMGRSFTGGV NVKF*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLTVSVVGKSRPRATS	SGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQA	HGTEQSVG	LET	TVSVVGKSRPRATS	SGLLHTS	
	10	20	30	40	50	60
m147.pep	40	50	60	70	80	90
	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
a147	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
	70	80	90	100	110	120
m147.pep	100	110	120	130	140	150
	GDMADFSPDHAIMVDTALSQQVEILRGPV	TLLYSSGNVAGLVDVADGKIPEKMPENGVS				
a147	GDMADFSPDHAIMVDSALSQQVEILRGPV	TLLYSSGNVAGLVDVADGKIPEKMPENGVS				
	130	140	150	160	170	180
m147.pep	160	170	180	190	200	210
	ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHAD				
a147	ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHAD				
	190	200	210	220	230	240
m147.pep	220	230	240	250	260	270
	TGSIGLSWVGEGKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL			
a147	TGSIGLSWVGEGKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL			
	250	260	270	280	290	300
m147.pep	280	290	300	310	320	330
	LTEEDIDYDNPGLSCGFHDDDDNAHA	HTHSGRPWIDLNRKRYELRAEWKQPFPGFEALRVH				
a147	LTEEDIDYDNPGLSCGFHDDDDNAHA	HTHSGRPWIDLNRKRYELRAEWKQPFPGFEALRVH				
	310	320	330	340	350	360
m147.pep	340	350	360	370	380	390
	LNRNDYRHDEKAGDAVENFFNNQT	ONARIELRHQPIGRKGSWGVQYLQOKSSALS	AISE			
a147	LNRNDYRHDEKAGDAVENFFNNQT	ONARIELRHQPIGRKGSWGVQYLQOKSSALS	SATSE			
	370	380	390	400	410	420
m147.pep	400	410	420	430	440	450
	AVKQPMLLDNKVQHYSFFGVEQANW	NFTLEGGVRVEKQKASIQYDKALIDRENYNHPL				
a147	AVKQPMLLDNKVQHYSFFGVEQANW	NFTLEGGVRVEKQKASIRYDKALIDRENYNHPL				
	430	440	450	460	470	480
m147.pep	460	470	480	490	500	510
	PDLGAHRQTARSFALSGNWFYTPQHK	LSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
a147	PDLGAHRQTARSFALSGNWFYTPQHK	LSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
	490	500	510	520	530	540
m147.pep	520	530	540	550	560	570
	HLNKERSNNIELALGYEGDRWQYNL	ALYRNRFNGNYIYAQT	LNDGRGPKSIEDDSEMKLVR			
a147	HLNKERSNNIELALGYEGDRWQYNL	ALYRNRFNGNYIYAQT	LNDGRGPKSIEDDSEMKLVR			

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	550	560	570	580	590	600
	580	590	600	610	620	630
m147.pep	YNQSGADFYGAEGEIFYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQ					
a147						
	610	620	630	640	650	660
	640	650	660	670	680	690
m147.pep	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147						
	670	680	690	700	710	720
	700	710	720	730		
m147.pep	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147						
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGctgg  ttcaTCCCGA
51  AgctATgagt  gtcggcgCGC  TTGccgAcaa  AATCCGCAAA  AtcgaAAact
101 gGCCGCAAAA  AGgcaTCTTA  TTCCACGACA  TCACGCCCCG  CCTGCAAAGT
151 GCGGAATACT  TCCGCCTTTT  GGTCGATTTG  CTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGCTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAaCGtcg  gctTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTAcg  cgcTCGAATA
351 CGGGGAAGCT  GCGGTGGAaA  TCCACACCGa  tgccgTCAAA  CCCGTTTCGC
401 GCGTCCTGCT  GGTCGATGAT  TTGGTTGCCA  CGGGCGGCAC  AATGCTTGCC
451 GGGCTGGAAC  TGATCCGCAA  ACTCGGCGGG  GAAATTGTCT  AAgccgccgC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGCGCAAGTG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGCAT  GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK
101 KGKLPFETVS  QSYALEYGEA  AVEIHTDAVK  PGRVLLVDD  LVATGGTMLA
151 GLELIRKLGG  EIVEAAAILE  FTDLQGGKNI  RASGAPLFTL  LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGCTGG  TTCATCCCGA
51  AGCTATGAGT  GTCGGCGCGC  TTGCCGACAA  AATCCGCAAA  ATCGAAAAC
101 GGCCGCAAAA  AGGCATCTTA  TTCCACGACA  TCACGCCCCG  CCTTCAAAGC
151 GCGGAATACT  TCCGCCTTTT  GGTGATTGTA  TTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGTTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAACGTCG  GTTTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTACG  CGCTCGAATA
351 CGGGGAAGCT  GCGGTGGAaA  TCCACACCGA  TGCCGTCAAA  CTCGGTTTCG
401 GCGTGCTGCT  GGTCGATGAT  TTGATTGCCA  CGGGCGGCAC  GATGCTTGCC
451 GGACTGGAAC  TGATCCGCAA  ACTCGGCGGA  GAAATTGTCT  AAGCCGCCGC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGTGAAGCG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGTAT  GAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK

```

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101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLVATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCGGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCCG	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAAA	CTCGGTTTCGC
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAGC	TGATCCGCAA	ACTCGGCGGG	GAAATTGTCT	AAGCCGCCGC
501	CATTTTGGA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCCTT	ATTTACCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LVNVGFVPIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

418

```

m148.pep      LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a148          LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
               70      80      90      100     110     120

               130     140     150     160     170     180
m148.pep      AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
               ||||||||||||||||:||||||||||||||||||||||||||||||||||
a148          AVEIHTDAVKLGSRVLLVDDLVATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
               130     140     150     160     170     180

               190     200
m148.pep      RASGAPLFTLLQNEGCMKGX
               ||||||||||||||||
a148          RASGAPLFTLLQNEGCMKGX
               190     200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1   ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGGTAC GACAAAGCAT TGATTGATCG AGAAAACCTAC
151 TACAACCAGC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAACCTCAGCC
251 TGACCGCCTC CCATCAGGAA cgCCTGCCGT CAACGCaagA actGtACgca
301 cacggcAAGC ACGtcgccac CAACACCTTT GAagtcggca acaaACACCT
351 CAACAAAGaG CgttccaacA atatcgaACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGAtT CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggacgC GGCCCAAAAT CCATCgaaga
501 cgacagcgaa ATGaagcTCG TGCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACGgcgcgga aggcgaaatc tACTTcaaaC CGAcACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCCT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCccttcaTC GCACAAGCCG
701 ACCAAACGC CCCCCGATT ccggctGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CGGTGCAAAc TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAAc gGGCCGCAGC TTtgccgGCg
1001 gcgtaAACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1   MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGDWRQYNL AAYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVS GDYVRGR LKNLPSLPGR EDPYGKRPFi AQADQNA PRI PAARLG FH LK
251 TSLTDRIDAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1   ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAACCTG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATTAGTAC GACAAAGCAT TGATTGATCG GGAAAACCTAC
151 TACAACCACC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAACCTCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACCTAC

```



```

451  ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501  CGACAGCGAA ATGAAGCTCG TGCCTACAA CCAATCCGGC GCCGACTTCT
551  ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601  GCGGTTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
651  ACCCGGCAGA GAAGATGCCT ACGGCAACCG TCCTTTCATC GCACAGGACG
701  ACCAAAAATGC CCCCCGTGTT CCGGCTGCGC GCCTCGGCTT CCACCTGAAA
751  GCCTCGCTGA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801  CGCCCCAAAC AAACCTGCCC GCTACGAAAC GCGCACGCCC GGACACCATA
851  TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901  AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCATCCG TTTACGCCCA
951  CAGCAGCTTT CTCTCTGATA CGCCGCAAAAT GGGCCGCAGC TTTACGGCGC
1001 GCGTGAACGT GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 598; ORF 149>:

m149.pep

```

1  MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEQKASIQY DKALIDRENY
51  YNHPLPDLGA HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDAYGNRPFI AQDDQNAPRV PAARLGPHLK
251 ASLTDRIAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 149 shows 95.9% identity over a 339 aa overlap with a predicted ORF (ORF 149.ng) from *N. gonorrhoeae*:

m149/g149

m149.pep	10	20	30	40	50	60
	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQASIQYDKALIDRENYNHPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANWDNFTLEGGVRVEKQASIRYDKALIDRENYNQPLPDLGA					
	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
g149	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
	RSNNIELALGYEGDRWQYNLALYRNRFNGYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
g149	RSNNIELALGYKGRWQYNLAAYRNRFNGYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLLKNLPSLPGREDAYGNRPFI AQDDQNAPRV					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLLKNLPSLPGREDPYGRPFIAQADQNAPRI					
	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
	PAARLGPHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHMLNLGAN YRRNTRYGEW					
g149	PAARLGPHLKSLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGAN YRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	310	320	330	340		
	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					

420

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX
 310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq
 1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTTCG GTGTAGAACA
 51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
 101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAACTAC
 151 TACAACCATC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
 201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAACCTAGCC
 251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
 301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAACACCT
 351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGCG
 401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC
 451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
 501 CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGT GCGGACTTCT
 551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
 601 GCGCTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
 651 ACCCGGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG
 701 ACCAAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA
 751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
 801 CGCCCCAAAAC AAACTCGCCC GCTACGAAAC GCGCACGCCC GGACACCATA
 851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
 901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACAATCCG TTTACGCCCA
 951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG
 1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep
 1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
 51 YNHPLPDLGA HRQTARFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
 101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGNY
 151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
 201 GVSVDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVHLK
 251 ASLTDRIAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW
 301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

m149/a149 98.8% identity in 339 aa overlap

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYQYDKALIDRENYNHPLPDLGA					
a149	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPLPDLGA					
	10	20	30	40	50	60
m149.pep	HRQTARFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	HRQTARFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	RSNNIELALGYEGDRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
a149	RSNNIELALGYEGDRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	130	140	150	160	170	180
m149.pep	RSNNIELALGYEGDRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
a149	RSNNIELALGYEGDRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	130	140	150	160	170	180
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDAYGNRPLIAQDDQNAPRV					
a149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDAYGNRPLIAQADQNAPRV					
	190	200	210	220	230	240
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDAYGNRPLIAQDDQNAPRV					
a149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDAYGNRPLIAQADQNAPRV					
	190	200	210	220	230	240
m149.pep	PAARLGFHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHMMLNLGANYYRRNTRYGEW					
a149	PAARLGFHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHMMLNLGANYYRRNTRYGEW					
	250	260	270	280	290	300

q149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTG	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACGGTCAG	CGTCGTCGGC	AAAAGCCGTC	CGCGCGCGAC	TTCCGGGGCTG
151	CTGCACACTG	CGACCGCTCT	GCACAAAATG	ATCTCCGGCG	ATACTTTGGCG
201	CCAAAAAGCC	GTCAACTTGG	GGCAGCGTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACGGCGGC	GGCGCATCCG	CTCCCGTTAT	TCGCGGCTCAA
301	ACGGGCAGAC	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	CGGGCGATAT
351	GGCGGACTTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTGCG
401	AACAGCTTGA	AATCTTCGCG	GGGGCGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGCTGGTGCA	TGTTGCCGAT	GGAAAAATCC	CGAAAAAAT
501	GCCTGAAAAC	GGCGTATCGG	GCGaagccgG	ATTGCGTTTG	AGCAGCGGCA
551	ATTTAGAAAA	ACTGCATATC	GCAGGATCA	ATATCGGACT	GGGCAAAAA
601	TTCTGTACTG	ATACCGAAGG	CTTGATCCGC	AAATCGGGCG	ATTACCGCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCTTGCC	CGACAGCCAT	CGCGATTTCG
701	AAACGGGCAG	CATCGGGCTG	TCTTGGGTGG	GCGAAAAAGG	CTTTATCGGC
751	GCAGCATACA	CGCACCCTCG	CGACCCTGAT	GGCCTGCCTG	CCCAACGCCA
801	CGAATACGAT	GATTGCCACG	CCGACATCAT	CTGGCAAAAG	AGTTTGATCA
851	ACAAACGCTA	TTTTCAGCTT	TATCCGCACT	TGTTGACCGA	AGAAGACATC
901	GATTACGCAC	ATCCGGGCTT	GAGCTCGCGT	TTCCACGACG	CGCAGCGGTG
951	ACACGCACAC	ACCCACAACG	GCAAACCGTG	GATAGACCTG	GCGCAACACG
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTGCGCGTAT	ATCTGAACCG	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCAGTA	GAAAACTTCT	TACAACAACA	AACACACAAC	CGCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCC	GCCATTTCGG	AAACCGTCCA
1251	ACAACCCGATG	TTGATTGACA	ACAATGTCCG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGCA	AGGATTGGGAC	AACTTGACGC	TTGAAGGCGG	GTACGCGGTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGGTACGAC	AAAGCATGTA	TTGATCGAGA
1401	AAACTACTAC	AACCGACCCC	TGCCCGACCT	CGGCGCGCAG	CGCCAAACGA
1451	CCCGCTCGTT	CGCACTTTTC	GGCAACTGGT	ATTTCACGCG	ACCAACACAA
1501	CTCAGCCTGA	CGCGCTCCCA	TCAGCAACGC	CTGCCGTCAA	CGCAAGAACT
1551	GTACGCCACG	GGCAAGCAGC	TCGCCACAATA	CACCTTTGAA	GTCCGCAACA
1601	AACACCTCAA	CAAGAGCGGT	TCCAACAATA	TGCAACTCGC	GCTGGGCTAC
1651	GAAGCGGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACATT	TACGCGAAAT	CTTTAAACGA	CGGACGCGCG	CCCAAAATCA
1751	TCGAAGACGA	ACGCGAAATG	AAGCTCGTGT	GCTACAACCA	TTCGGTGGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCAATCGT	GTTTCCGGCG	ACTATGTACG	AGGCCGCTCG	AAAAAAGCTG
1901	CGTCCCTACC	CGGACGGGAA	GATCCCTACG	GCAAAAGTCC	CTTCATCGCA
1951	CAAGCCGACC	AAAAGGCCCC	CGCATATTCC	GCTGCGCGCC	TCGGGTTCCA
2001	CCTGAAAACC	TCGCTTAACC	ACCGTATCGA	TGCCAATTGT	GACTACTACC
2051	CGGTGTTTCG	CCAAAACAAA	CTCGCCCGCT	ACGAAACGCG	TACGCCCGGA
2101	CACCATATGC	TCAACTTCGG	TGCAAACTAC	CGCCGCAATA	CGCGCTATGG
2151	CGAGTGGAA	TGGTACGTCA	AAGCGACAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCCCACG	CAGCTTCTCT	TCTGATACGC	CGCAAAATGG	CCGACGCTTT
2251	ACCGGCGGCG	TAAACGTGAA	GTTTTTAA		

g149-1.pep

1	MAQITLKPIV	LSILLINTPL	LAQAHETEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDVT	PGHASQYGG	GASAPVIRSG
101	TGRRIKVLNH	HGETGDMADF	SPDHAIMDVT	ALSQQVEILR	GPVTLTYSGG
151	NVAGLVDVAD	GKIPEKMPEN	GVSGEAGLRL	SSGNLEKITS	AGINIGLGKN
201	FVLHTEGLRY	KSGDYAVPRY	RNLKRLPDSH	ADSQTSGIGL	SWVGEGKFGI
251	AAYSDRRDRY	GLPAHSHEYD	DCHADLIWQK	SLINKRYLQL	YPHLLTEEDI
301	DDYNPLSCSG	FHDGDGAHAH	THNGKPWIDL	RNKRYELRAE	WKOPFFGEFA

```

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AIPETVQOPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFNGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DPYGKRPFIA
651 QADQNAPRIP AARLGFHLKT SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

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1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCG CTCCCCTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGGGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAA GCGGTATCGG GCGAACTCGG ATTGCGTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCGGT
651 ACCGCGTTAC CGCAATCTGA AACGCGTGCC CGACAGCCAC GCCGATTGCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCGTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAAACGCTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAAC TCCGTGCCGAA TGGAAGCAAC CGTTCGCCGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGGCCCA CCAACCCATA GGTCTGCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTTAA
1251 ACAACCGATG CTGCTTGACA ACAAAAGTGA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATGGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTAC AACCACCCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTCG GGCAACTGGT ATTTACGCCC ACAACACAAA
1501 CTCAGCGCTG CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAAACAG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTCAT TACGCCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGGCG ACTATGTACG AGGCGGTCTG AAAAACCTGC
1901 CTTCCTTACC CGGCAGAGAA GATGCCTACG GCAACCGTCC TTTATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAAC TAC GCGCGTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCTC TCTGATACG CGCAATGGG CCGCAGCTTT
2251 ACCGGCGGCG TGAACGTGAA GTTTTAA

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This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

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1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSGLGLRL SSGNLEKLTG GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 VAYSDDRRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSGC FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQFPFGFEA
351 LRVHLNRNDY HHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AISEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

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551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGREDAYGNRPFFIA
651 QDDQNAPRVP AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

m149-1.pep	10	20	30	40	50	60
	MAQTTLKPIVLSILLINTPLLAQAHETE	QSV	DLET	VS	VVGKSRPRAT	SGLLHTSTASDKI
g149-1	MAQITLKPIVLSILLINTPLLAQAHETE	QSV	GLET	VS	VVGKSRPRAT	SGLLHTSTASDKI
	10	20	30	40	50	60
m149-1.pep	70	80	90	100	110	120
	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
g149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
	70	80	90	100	110	120
m149-1.pep	130	140	150	160	170	180
	SPDHAIMVDTALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL			
g149-1	SPDHAIMVDTALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS	GEAGLRL			
	130	140	150	160	170	180
m149-1.pep	190	200	210	220	230	240
	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNLKRLPDSHAD	SQTGSIGL			
g149-1	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNLKRLPDSHAD	SQTGSIGL			
	190	200	210	220	230	240
m149-1.pep	250	260	270	280	290	300
	SWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI				
g149-1	SWVGEKGFIGAAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI				
	250	260	270	280	290	300
m149-1.pep	310	320	330	340	350	360
	DYDNPGLSCGFHDDNAHAHT	SGRPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY				
g149-1	DYDNPGLSCGFHDGGAHAHT	NGKRPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY				
	310	320	330	340	350	360
m149-1.pep	370	380	390	400	410	420
	RHDEKAGDAVENFFNNQ	TQNARIELRHQPIGRKGSWGVQYLQOKSSALSAISEAVKQPM				
g149-1	HHDEKAGDAVENFFNNK	THNARIELRHQPIGRKGSWGVQYLQOKSSALSAIPETVQQPM				
	370	380	390	400	410	420
m149-1.pep	430	440	450	460	470	480
	LLDNKVQHY	SFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENYNHPDLGAH				
g149-1	LIDNNVRHY	SFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNQPLDLGAH				
	430	440	450	460	470	480
m149-1.pep	490	500	510	520	530	540
	RQTAR	SFALSGNWFYTPQHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER			
g149-1	RQTAR	SFALSGNWFYTPHHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER			
	490	500	510	520	530	540
m149-1.pep	550	560	570	580	590	600
	SNNIELALGYEGDRWQYN	LALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
g149-1	SNNIELALGYEGDRWQYN	LAAAYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
	550	560	570	580	590	600
m149-1.pep	610	620	630	640	650	660
	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGREDAYGNRPFFIAQDDQNAPRVP				
g149-1	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGREDPYGKRPFIAQADQNAPRIP				
	610	620	630	640	650	660

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	670	680	690	700	710	720
m149-1.pep	AARLGFLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
g149-1	AARLGFLKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
	670	680	690	700	710	720
	730	740	750	759		
m149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

a149-1.seq

```

1  ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTAATCAA
51  CACACCCCTC CTCTCCCAAG CGCATGGAAC TGAGCAATCA GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC TTCGGGGCTG
151 CTGCACACTT CTACCGCCTC CGACAAAATC ATCAGCGGCG ACACCTTGCG
201 ACAAAAAGCC GTCAACTTGG GTGATGCTTT AGACGGCGTA CCGGGCATTC
251 ATGCCTCGCA ATACGGCGGC GGCGCATCCG CTCCCGTTAT TCGCGGTCAA
301 ACAGGCAGAC GGATTAAAGT GTTGAACCAT CACGGCGAAA CGGGCGACAT
351 GGCGGACTTC TCTCCAGACC ATGCAATCAT GGTGGACAGC GCCTTGTCGC
401 AACAGGTCTG AATCCTGCGC GGTCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGGCCGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGAATCGG ATTGCGTTG AGCAGCGGCA
551 ATCTGGAAAA ACTCACGTCC GGCGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AACGCCTGCC CGACAGCCAC GCCGATTCGC
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATTA
851 ACAAACGCTA TTTGCAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTTCACGACG ACGATGATGC
951 ACACGCCCAT GCCACAACG GCAAACCTTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACT CCGCGCCGAA TGGAAGCAAC CGTCCCCGG TTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTA GAAACTTTT TTAACAACCA AACGCAAAAC GCCCGTATCG
1151 AGTTGCGCCA CCAACCCATA GGCCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTGGGAC AAAATCCAG TGCTTTATCT GCCACATCCG AAGCGGTCAA
1251 ACAACCGATG CTGCTTGACA ATAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATGGGAC AACTTCACGC TTGAAGGCGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT CCGCTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTAC AACCATCCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCGGCTCAT CGCACTTTCG GGCAACTGGT ATTTACGCC ACAACACAAA
1501 CTCAGCTGA CCGCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC CTTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 CAACTACATT TACGCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGTGGC
1801 GACTTCTACG CGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGGGAA GACGCCTACG GCAACCGCCC ACTCATTGCC
1951 CAAGCCGACC AAAACGCCCC TCGCGTTCCG GCTGCGCGCC TCGGCGTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGCATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGCGGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

a149-1.pep

```

1  MAQTLKPIV LSILLINTPL LSOAHGTEQS VGLETSVVG KSRPRATSGL
51  LHTSTASDKI ISGDTLROKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDS ALSQQVEILR GPVTLTYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSGLGLRL SSGNLEKLTG GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 AAYSDDRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLSCG FHDDDDAH AHNGKPWIDL RNKRYELRAE WKQFPFGFEA

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351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTQN ARIELRHQPI GRLKGSWGVSQ
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NHPPLDLGAH RQTARSFALS GNWYFTPOHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSPGREG DAYGNRPLIA
651 QADQNAAPRV AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQA	HGTEQSVGLET	SVVVGKSRPRATS	GLLHTSTASDKI		
m149-1	MAQTTLKPIVLSILLINTPLLAQA	HETEQSVDELET	SVVVGKSRPRATS	GLLHTSTASDKI		
	10	20	30	40	50	60
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRI	KVLNHHGETGDMADF			
m149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRI	KVLNHHGETGDMADF			
	70	80	90	100	110	120
	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKIPEK	MPENGVS	GELGLRL		
m149-1	SPDHAIMVDTALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKIPEK	MPENGVS	GELGLRL		
	130	140	150	160	170	180
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNLK	RLPDSHAD	QTSIGL		
m149-1	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNLK	RLPDSHAD	QTSIGL		
	190	200	210	220	230	240
	250	260	270	280	290	300
a149-1.pep	SWVGEKGFIGAAYS	DRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHLLTEEDI			
m149-1	SWVGEKGFIVAYS	DRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHLLTEEDI			
	250	260	270	280	290	300
	310	320	330	340	350	360
a149-1.pep	DYDNPLGLSCGFHDDDAHAHAH	NGKPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
m149-1	DYDNPLGLSCGFHDDDAHAHAH	THSGRPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
	310	320	330	340	350	360
	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTQN	ARIELRHQPIGRLKGSWGVSQY	LQKSSALSATSEAVKQPM			
m149-1	RHDEKAGDAVENFFNNQTQN	ARIELRHQPIGRLKGSWGVSQY	LQKSSALSATSEAVKQPM			
	370	380	390	400	410	420
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDN	FTLEGGVRVEKQKASIRYD	KALIDRENYNHPPLDLGAH			
m149-1	LLDNKVQHYSFFGVEQANWDN	FTLEGGVRVEKQKASIQYD	KALIDRENYNHPPLDLGAH			
	430	440	450	460	470	480
	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGN	WYFTPOHKLSLTASHQERLP	STQELYAHGKHVATNTFEV	GNKHLNKER		
m149-1	RQTARSFALSGN	WYFTPOHKLSLTASHQERLP	STQELYAHGKHVATNTFEV	GNKHLNKER		
	490	500	510	520	530	540
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYN	LALYRNRFGNYIYAQTLNDGRG	PKSIEDDSEM	KLVRYNQSGA		
m149-1	SNNIELALGYEGDRWQYN	LALYRNRFGNYIYAQTLNDGRG	PKSIEDDSEM	KLVRYNQSGA		
	550	560	570	580	590	600
	610	620	630	640	650	660

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a149-1.pep  DFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPLIAQADQNAPRVP
              |||
m149-1       DFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFFIAQDDQNAPRVP
              610      620      630      640      650      660

              670      680      690      700      710      720
a149-1.pep  AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN
              |||
m149-1       AARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN
              670      680      690      700      710      720

              730      740      750      759
a149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              |||
m149-1       WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              730      740      750

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

```

g150.seq (partial)
1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTTGA
101 GCGGTTTCGGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCCTGCCG GTTGCCTCCG
251 CACTGTTATC CCATTTTCGAA CTCACGCAAA ACACCCCGCG CTTTGTCAAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAATTCTC CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTTCGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCGTTTC GAACACGAAG
551 GGCGCGCCAG GGCGGGCGGC GCATCGGGTT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCCGC AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATCGGGCAAA AATGGCAAAA GAAGTGGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCGG GGCATTGCGA CGAAGACGGC
1051 GCAGAAAGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

```

g150.pep (partial)
1  ..YCKADPFPA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAGGKTLV VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHFRPAK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIMVIGS GTGVAPFRAF VQQRAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDFG LHRYPFAWSR DQEEKIYVQD
301 KIREQAEGLW OWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDEDEG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

```

m150.seq
1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCACGCA
51  GCTCCTGTCG GGGCTGGACG CGGCACAATG GGCGTGCGTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGCAGA ACCTTTTTCG GTAACCGTCC TTTCCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCGG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGGCGAACG CCGCCTGCTG CTGGTTACCT CCACCCAGG
351 CGAAGGCGAA CCGCGAAAG AAGCCGTCTG GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAAACTCC AATTTCCTGT ACTGGGTTTG

```



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451 GCGGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
501 GCGTTTTGAA GAATTGGGCG CAAAACGGCT GCTCGAACGC GTTGATGCGG
551 ATTTGGACTT TACCGCCTCC GCAAACGCCT GGACAGATAA TATCGCCGCA
601 CTCTTAAAG AAGAAGCCGC AAAAAACCGG GCAACGCCCG CGCCGCAGAC
651 AACGCCCCC GCGGCGCTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701 CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCCGC
751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGGA GCGGTTCCGA
801 TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
851 CGGCACTGGT CAGGGAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
901 GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGCGCGCG CACTTTCATC
951 TCATTTGCAA CTCACGCAA ACACCTCCGC TTTCGTCAA GGCTATGCCG
1001 CGTTCGCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
1101 CCCGGCAAGC CTGACGGCAG AACAATTCAT CCGTTTACTG CGTCCGCTTG
1151 CACCCCGTTT GTATTCGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
1201 GTGCATTTAA CTGTCGGCGT GGTTTCGTTT GAACACGAAG GCCGCGCCAG
1251 AACGGGCGGC GCATCGGGTT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGCGC TCGCACCGTT
1401 CCGCGCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAAAC
1451 GGCTGATTTT CCGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGGT ACGATTTTCG
1551 CTGGTCCCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
1701 GGATGTGATT ATCGGGGCG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

```

1  MQNTNPPLPP LPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51  TALPAAEFPS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERRLL LVTSTQEGEG PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
201 LLKEEAAKNR ATPAPQTTPP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
251 QSKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
301 EIQAGGKMMP VARALSSHFE LTQNTPAFVK GYAAFAHYEE LDKIIADNAV
351 LQDFVQNTPI VDLVHRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
401 VHLTVGVVRF EHEGRARTGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
451 SRKPIVMIGS GTGVAPFRAF VQQRAAENAE GKNWLI FGNP HFARDFLYQT
501 EWQQFAKDG F LHRDYFAWSR DQEEKIYVQD KIREQAELGW QWLQEGAHY
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

```

                210      220      230      240      250      260
m150.pep      LLKEEAAKNRATPAPQTTPPAGLQTAPDGRYCKAAPFPAALLANQKITARQSDKDVRHIE
                |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
g150                YCKADPFPAALLANQKITARQSDKDVRHIE
                10      20      30

                270      280      290      300      310      320
m150.pep      IDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPATEIQAGGKMMPVARALSSHFE
                |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
g150                IDLSGSDLHYLPGDALGVWFDNDPALVGEILDLLGINPATEIQAGGKTLVASALLSHFE
                40      50      60      70      80      90

                330      340      350      360      370      380
m150.pep      LTQNTPAFVKGYAAFAHYEELDKIIADNAVLDQDFVQNTPIVDVLHFRFPASLTAEQFIRLL

```

a150.seq

a150.seq	1	ATG	CAG	AACA	CAA	ATC	CGC	CGC	ATT	ACC	GCCT	ATG	CCG	CCCC	AA	ATC	ACG	CA
51	GCT	CCT	GT	CG	GGG	CCT	GG	ACG	CGG	CACA	AA	TGG	CGT	TGG	CT	TCC	GGT	TAC
101	CTT	GGG	CAAA	AG	CAG	GAA	AA	CGG	CAT	CTG	CAG	GAT	TGC	C		CGC	GCT	TAC
151	ACG	GCAT	TG	C	GAC	GGC	GAG	A	ACCT	TTTT	TCC	GTA	ACC	GT	C	TTT	CCG	CCT
201	GCAA	ACCG	GC	AAT	GCG	AAAT		CCG	TG	GCC	G	CAA	AGC	GGC	G	GAC	AGC	TG
251	AAG	CGCC	CG	CAT	CCA	AGT	C	AGT	CGC	GC	CG	AAC	TGA	AAG	A	CTA	TAA	GGC
301	AAAA	CAT	CG	CCG	CG	GAA	CG	CGC	CT	GT	CTG	CTG	GT	TAC	CT	CA	CC	CAAG
351	CGA	AGG	CGAA	CCG	CCG	GAA	G	AAG	CGT	CGT	GCT	GC	ACA	AA		CTG	CT	GAAC
401	GCA	AAAA	AAG	C	CCG	GAAT	TG	GACA	AACT	CC	AAT	TG	CCG	T		ACT	GGG	TTT
451	GGC	GAC	AG	CT	TAT	CC	GAA	TTT	CT	GCC	G	GCG	GGC	AA	A	ATT	T	CGACA
501	ACG	TTT	TGAA	GA	ATT	TGG	GCG	CAAA	AC	GC	CT	GCT	CGA	AC	G	GTT	GAT	TGCG
551	ATT	TG	GACT	TG	CCG	CCG	CC	G	CAG	AC	GGT	GG	CAG	ATA	A	TAT	CG	CCGA
601	CTC	TTAA	AA	AAGA	AG	CCG	C	AAAA	AC	CCG	G	GA	AC	CCG	C	CGC	CG	CAG
651	AAC	GC	CCCC	G	CCG	CCG	CT	AG	AC	GGC	ACC	GGA	TG	G	CAG	TAC	T	GCAAG
701	CAG	AC	CCCT	T	CCG	CCG	CC	CTG	CT	GG	CCA	ATC	AG	AAAT	A	CAC	CG	CCG
751	CAAT	CC	GATA	AAG	AC	TG	CG	CC	CAT	CG	AA	ATC	GAT	TTT	G	GCG	GT	CGGA
801	TTT	G	CACT	AG	CT	CCG	GGG	AC	G	CGT	CTCG	CG	CTT	TG	TTT	GAC	A	CACT
851	CGG	CACT	GT	CAGG	GAA	AT	C	CTA	GAC	CTG	C	TGG	CAT	CG	A	TAC	GG	CAAC
901	GAA	ATAC	AG	CGG	CGG	GAAA	A	AA	CCCT	GCCG		GTT	GC	CTCCG	C	CACT	GTT	ATC
951	CCAT	TTT	TGAA	CTC	ACG	CAAA	A	AC	AC	CC	CCG	CTT	TG	TCAA	A	GG	CTAT	GCCC
1001	CGT	T	CGCC	GA	TGAT	GAC	GAA	CTC	G	ACC	CGT	TTG	CT	GCC	GA	CA	AC	CGCGTT
1051	TTG	CA	AGG	CT	TTG	TG	CAAA	CAC	G	CCG	GAT	GCC	GAT	GTG	C	TG	CA	CGCTT
1101	CCC	GGG	CAAA	CTG	ACG	CGG		AA	CAAT	TCG	C	GGC	CT	TACTG	C	CGC	CCG	CTT
1151	CGC	CGC	G	CT	ATT	CG	GAT	T	CTC	CTG	CTG	AGG	CGG	AA	GT	GGG	G	ACGAA
1201	GTG	CAC	CTGA	CCG	T	CGG	CGC	G	GTG	CGT	TTT	GAA	CAC	G	AA	GGC	G	CCAG
1251	GGC	GGG	CGG	G	CAT	CGG	T	T	CCT	TG	CCG	A	CGG	CTG	GAA	GAG	G	ACGCA
1301	CGG	TG	CGCGT	G	TTT	TG	GGAA	CG	CA	ACG	ACG	G	CTT	C	AGG	G	CC	CAAG
1351	AGC	CG	CAAG	C	GAT	TG	TGAT	GAT	CGG	CTCG		GGC	AC	CGG	C			

1701 GGATGTGATT ATCGGGGCAG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
 1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTTATTGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep
 1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
 51 TALPTAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
 101 KNIAGERRLL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL
 151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA
 201 LLKEEAANKR ATPAPQTTPP AGLQTAPDGR YCKADPFPAAL LANQKITAR
 251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDQAT
 301 EIQAGGKTLF VASALLSHFE LTQNTPAFVK GYAPFADDDDE LDRIAADNAV
 351 LQGFVQSTPI ADVLHRFPFAK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE
 401 VHLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
 451 SRKPIVMIGS GTGVAPFRAF VQRAAENAE GKNWLFNGNP HFARDFLYQT
 501 EWQQFAKDGFLHRYDFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHIY
 551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

m150/a150 94.8% identity in 599 aa overlap

	10	20	30	40	50	60
m150.pep	MQNTNPPLPP	MPPEITQLLS	GLDAAQWAWL	SGYAWAKAGN	GASAGLPALQ	TALPAAEPFS
a150	MQNTNPPLPP	MPPEITQLLS	GLDAAQWAWL	SGYAWAKAGN	GASAGLPALQ	TALPAAEPFS
	70	80	90	100	110	120
m150.pep	VTVLSASQTG	NAKSVADKAA	DSLEAAGIQV	SRAELKDYKA	KNIAGERRLL	LVTSTQGEGE
a150	VTVLSASQTG	NAKSVADKAA	DSLEAAGIQV	SRAELKDYKA	KNIAGERRLL	LVTSTQGEGE
	130	140	150	160	170	180
m150.pep	PPKEAVVLHK	LLNGKKAPKL	DKLQFAVLGL	GDSSYPNFCR	AGKDFDKRFE	ELGAKRLLER
a150	PPKEAVVLHK	LLNGKKAPKL	DKLQFAVLGL	GDSSYPNFCR	AGKDFDKRFE	ELGAKRLLER
	190	200	210	220	230	240
m150.pep	VDADLDFASA	NATDNIALL	KEEAANKRAT	PAPQTTPP	AGLQTAPDGR	YCKAAPPFAA
a150	VDADLDFAAA	ADGWTDNIA	ALLKEEAANKR	ATPAPQTTPP	AGLQTAPDGR	YCKADPFPAAL
	250	260	270	280	290	300
m150.pep	LLANQKITAR	QSDKDVRHIE	IDLSGSDLHY	LPGDALGVWF	DNDPALVREI	LDLLGIDPAT
a150	LLANQKITAR	QSDKDVRHIE	IDLSGSDLHY	LPGDALGVWF	DNDPALVREI	LDLLGIDQAT
	310	320	330	340	350	360
m150.pep	EIQAGGKMMP	VARALSSHF	ELTQNTPAF	VKGYAAFAH	EELDKIADNA	VLQDFVQNTPI
a150	EIQAGGKTLF	VASALLSHF	ELTQNTPAF	VKGYAPFADD	DELDRIAADNA	VLQGFVQSTPI
	370	380	390	400	410	420
m150.pep	VDVLRFPASL	TAEQFIRLL	RPLAPRLYSI	SSAQAEVGDE	VHLTVGVVRF	EHEGRARTGG
a150	ADVLHRFPFA	KLTAEQFAGL	LRPLAPRLYSI	SSSQAEVGDE	VHLTVGAVRF	EHEGRARAGG
	430	440	450	460	470	480
m150.pep	ASGFLADRLE	EDGTVRVF	VERNDGFR	LPEDSRKPI	VMIGSGTG	VAPFRAFVQRAAENAE
a150	ASGFLADRLE	EDGTVRVF	VERNDGFR	LPEDSRKPI	VMIGSGTG	VAPFRAFVQRAAENAE
	490	500	510	520	530	540
m150.pep	GKNWLIFGNP	HFARDFLYQ	TEWQQFAK	DGFLHRYD	FAWSRDQEE	KIYVQDKIREQAEGLW

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a150      GKNWLFFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQDKIREQAEGW
           490      500      510      520      530      540

           550      560      570      580      590      600
m150.pep  QWLQEGAHIVCGDAAKMAKDVEAALLDVIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           |||||
a150      QWLQEGAHIVCGDAAKMAKDVEAALLDVIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1   ATGAAACAAA   TCCGCAACAT   CGCCATCATC   GCACACGTCG   ACCACGGCAA
51  AACCACATTG   GTCGACCAAC   TGCTGCGCCA   ATCCGGCACA   TTCCGCGCCA
101 ACCAGCAGGT   TGACGAGCGC   GTGATGGACA   GCAACGACCT   TGAAAAAGAA
151 CGCGGCATCA   CCATCCTCGC   CAAAAACACC   GCCATCGATT   ACGAAGGCTG
201 CCACATCAAT   ATCGTCGACA   CGCCGGGACA   CGCCGACTTC   GGCGGCGAAG
251 TGGAGCGCGT   TTTGGGGATG   GTGGATTGCG   TCGTCTTGTT   GGTGGACGCA
301 CAGGAAGGTC   CGATGCCGCA   AACCCGTTTC   GTGACCAAAA   AAGCCTTGCG
351 TTTGGGGCTG   AAACCGATTG   TCGTCATCAA   CAAAATCGAC   AAACCGTCCG
401 CCCGTCCGAG   CTGGGTTATC   GACCAGACTT   TCGAGTTGTT   CGACAACTTG
451 GGTGCGACCG   ACGAGCAGTT   GGATTTCCTG   ATGTGTTACG   CTTCAGGTTT
501 GAGCGGCTTT   GCCAAGCTGG   AAGAAAacga   CGAGAGCAGC   GATATGCCCC
551 CGCtggttcga   CACCATCCTA   AAATACAcgc   ctgCACCAGG   CGGCAGCGCG
601 GACGAGCCGC   TGCAACTGCA   AATTTCCCAA   CTCGACTACG   ACAACTACAC
651 CGGCCCGCCT   GGTATCGGTC   GTATCTTGAA   CGGACGCATC   AAACCCGGCC
701 AAACCGTTGC   CGTGATGAAC   CACGAGCAGC   AAATCGCCCA   AGGCCGCATC
751 AACCAGCTTT   TGGGTTTCAA   AGGCTTGGA   CGCGTGCCGC   TTGAAGAAGC
801 CGAAGCCGGC   GACATTGTGA   TTATTTCCGG   TATCGAAGAC   ATCGGCATCG
851 GCGTAACCAT   CACCGACAAA   GACAACCCCA   AAGGCTGCC   GATGTTGAGC
901 GTGGACGAAC   CGACGCTGAC   GATGGACTTT   ATGGTAAACA   CCAGCCCGCT
951 CGCAGGTACA   GAAGGCAAAT   TCGTGACCAG   CCGCCAAATC   CGCGACCGCC
1001 TGCAAAAAGA   ATTGCTGACC   AACGTTGCC   TGCGCGTGGA   AGACACCGCC
1051 GatgCCGACG   TGTTCCGCGT   ATCcgGGCGC   GGCGAACTGC   ACCTGACGAT
1101 TTTGCTGGAA   AATATGCGCC   GCGAAGGCTA   CGAACTCGCC   GTCGGCAAGC
1151 CGCGCGTCGT   GTACCGAGAC   ATCGACGGTC   AAAAATGCGA   ACCTTATGAA
1201 AACCTGACTG   TGGACGTACc   cgacgacAAC   CAAGGCGCGG   TAATGGAAGA
1251 ACTCGGCCGC   CGCCGTGGCG   AACTGACCAA   TATGGAAGC   GACGGCAACG
1301 GacgCACCCG   CCTCGAATAC   CATATTCCAG   CGCGCGGCTT   GATCGGTTTC
1351 CAAGCGAAT   TCATGACCCT   GACGCGCGGC   GTCGGGCTGA   TGAgccacGT
1401 GTTcgacgac   tacgcgcccg   tcaAACCCGA   TATGCCCCGC   CGCCACAACG
1451 GCGTactggt   GtcccaAGAG   CAGGGCGAGG   CGGTTGCTTA   CGCCTTGTGG
1501 AATCTTGAAG   ACCGCGGCCG   TATGTTGTA   TCGCCCAACG   ACAAATCTA
1551 CGAAGGTATG   ATTATCGGCA   TCCACAGCCG   CGACAACGAT   TTGGTGGTCA
1601 ACCCGCTCAA   AGGCAAAAAA   CTCACCAATA   TCCGTGCCAG   CGGTACCGAC
1651 GAAGCGGTGC   GCCTGACCAC   GCCGATCAAA   CTGAcgcTGG   AAGGCGCGGT
1701 CGAGTTTATC   GACGATGACG   AGCTGGTGGA   AATCACGCCG   CAAtccatcc
1751 gcctgcgcat   gcgttacctG   AGCGaattgg   aacgccgccc   tcaTTTTAAA
1801 AagctgGATT   AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1   MKQIRNIAII  AHVDHGKTTL  VDQLLRQSGT  FRANQQVDER  VMDSNDLEKE
51  RGITILAKNT  AIDYEGCHIN  IVDTPGHADF  GGEVERVLGM  VDCVLLVDA
101 QEGMPQTRF  VTKKALALGL  KPIVVINKID  KPSARPSWVI  DOTFELFDNL
151 GATDEQLDFP  IVYASGLSGF  AKLEETDESS  DMRPLFDTIL  KYTPAPSGSA
201 DEPLQLQISQ  LDYDNYTGRL  GIGRILNGRI  KPGQTVAVMN  HEQQIAQGRI
251 NQLLGFKGLE  RVPLEBAEAG  DIVIISGLED  IGIGVTITDK  DNPKGLPMLS
301 VDEPTLTMDF  MVNTSPLAGT  EGKFVTSRQI  RDRLQKELLT  NVALRVEDTA
351 DADVFRVSGR  GELHLTILLE  NMRREGYELA  VGKPRVVYRD  IDGQKCEPYE
401 NLTVDPDDN  QGAVMEELGR  RRGELTNMES  DGNRTRLEY  HIPARGLIGF
451 QGEFTLTRG  VGLMSHFDD  YAPVKPDMGP  RHNGVLVSQE  QGEAVAYALW

```

431

501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHFK
 601 KLD*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
 51 AACACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
 251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG
 401 CTCGTCCGAG CTGGGTATC GACCAAACTT TCGAGCTGTT CGACAACTTG
 451 GGCAGCAGCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTTCAGGGTT
 501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
 651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
 701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
 751 AACAGCTTT TGGGTTTCAA AGGTTTGAA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATCGAAGAC ATCGGTATCG
 851 GCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
 951 GCGGGGTACG GAAGGCAAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
 1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GCGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
 1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
 1351 CAAGGCGAAT TTATGACCTT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
 1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTTG
 1501 AACTTGGAAG ACCCGGCGCG TATGTTGTA TCGCCCAACG ACAAATCTA
 1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
 1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAAA
 1801 AAGCTGGATT GA

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQOQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HDQQIAQGRI
 251 NQLLGFKGLF RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVFDG YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

	10	20	30	40	50	60
m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMDSDNLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMDSDNLEKERGITILAKNT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m151.pep	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m151.pep	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m151.pep	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m151.pep	HDQQIAQGRINQLLGFKGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	:					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m151.pep	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
	310	320	330	340	350	360
	370	380	390	400	410	420
m151.pep	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQAVMEELGR					
	370	380	390	400	410	420
	430	440	450	460	470	480
m151.pep	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m151.pep	RHNGVLVSQEQGEAVAYALWNLEDGRGMFVSPNDKIYEGMIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDGRGMFVSPNDKIYEGMIGIHSRDNDLVNPLKGKK					
	490	500	510	520	530	540
	550	560	570	580	590	600
m151.pep	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					
	550	560	570	580	590	600

433

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA
 51 AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGT TGGTGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGGC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAAATCGAC AAACCGTCCG
 401 CCCGTCCGAG CTGGGTCAAT GACCAAACTT TCGAGCTGTT CGACAACCTG
 451 GGCGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTTGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
 651 CGGCGCGCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGATC
 751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
 951 GGCAGGTACG GAAGGCAAAT TCGTAACCG CCGCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
 1051 GATGCCGACG TGTTCGCGCT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGCCGCG CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
 1301 GACGCACCCG CCTCGAATAC CATATCCAG CGCGCGGCTT GATCGGCTTC
 1351 CAAGGCGAAT TTATGACCTT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
 1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
 1501 AATCTGGAAG ACCGCGGCCG TATGTTGTA TCGCCCAACG ACAAATCTA
 1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCGATTAG CTGACGCTGG AAGGTGCGGT
 1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
 1801 AAGCTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQAQGR
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLTILE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVFD YAPVKPMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

m151/a151 99.8% identity in 603 aa overlap

10

20

30

40

50

60

434

```

m151.pep      MKQIRNIAIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151          MKQIRNIAIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
              10      20      30      40      50      60

              70      80      90      100     110     120
m151.pep      AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
a151          AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m151.pep      KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
a151          KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
              130     140     150     160     170     180

              190     200     210     220     230     240
m151.pep      DMRPLFDTILKYTPAPSGSADETLLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
a151          DMRPLFDTILKYTPAPSGSADETLLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
              190     200     210     220     230     240

              250     260     270     280     290     300
m151.pep      HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
a151          HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
              250     260     270     280     290     300

              310     320     330     340     350     360
m151.pep      VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR
a151          VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR
              310     320     330     340     350     360

              370     380     390     400     410     420
m151.pep      GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR
a151          GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR
              370     380     390     400     410     420

              430     440     450     460     470     480
m151.pep      RRGELTNMESDGNGRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG
a151          RRGELTNMESDGNGRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG
              430     440     450     460     470     480

              490     500     510     520     530     540
m151.pep      RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGKK
a151          RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGKK
              490     500     510     520     530     540

              550     560     570     580     590     600
m151.pep      LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
a151          LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
              550     560     570     580     590     600

m151.pep      KLDX
a151          KLDX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aACCAaagt ctgGGacttc cCacccgcc ttTTCactG
51 GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```


g152.pcp

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

m152.seq

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

m152.pap

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/q152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	:					
g152	MKNKTKVWDFPTRLFWHLLAASLPFMWYSAKAGGDMQLQWHTRVGLLVFLFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:					
g152	GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAVAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAIILLSX			
	:			
g152	TGFKYIEGKTSIRFAGKAALAAALSVAAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
  1  ATGAAAAACA AAACCAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
 51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101  GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151  CTCGTATTCC GCCTCTGCTG GGGCATTGCG GGCAGCGATA CCGCCCGTTT
201  CTCCCGTTTC GTCCGCGGAT GGTGCGGTAT CAGAGAGTAT ATGAAAAACG
251  GTATTCCCGA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCAGTGATG
301  GTCGTTGCGC TTTTGGCCGC CGTGTGCTTC CAAGTCGGCA CAGGGCTTTT
351  TGCCGCCGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGGG
401  TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451  AAAGTGTCTG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501  CCGCGTGTTT AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551  AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601  GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651  GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
  1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFILEFL
 51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101  VVALLAAVSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151  KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201  AAALSVAALA AAAIILLS*

```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGDMLQWHTRVGLFVLFLLVFRLCWGIW					
	: : : :					
a152	MKNKTKVWDFPTRLFHWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILFLLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKKNLVLPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAIILLSX			
	:			
a152	TGFKYIEGKTSIRFAGKAALAAALSVAAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

g153.seq

```

1 atgggggtttg cttacAgat gacgtatatc gaggtCGGga taccggaggc
51 ggcacccgctc ctttCgctGC CCGAGATgat gcgcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TGctgaCTTT cGGCGcgcCG
151 GTTCTGTTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTCCGC CTGTCGGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCAA ATCGGCGGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTtccg
501 cgacAGTgcc gaatccCCCT GCGGGGTGTg cgGCGcggaa CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCTgac ggcggcggtT
601 GTTTTGTATT TCCctgCcaa TATCctgccc attaTGAttt cgtccAATCc
651 tgcgcgccag GAGGcCAACA CCATCTTTAG CGGCATCGCT TATATGTGGG
701 ACGAGGCTCT CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGGCGGCACG
801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCCaCaC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTTT GACGATGCTG TCCGCCTATT
1001 ATTTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

g153.pep

```

1 MGFAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51 VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAPFLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGNNAV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYGGRPKSL S ISSAFLTA AV
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDR LI AAVIFSAS IL
251 VPVLKIAAMS VLIAAARFAL PAGAKKLSHL YRITEAVGRW SMIDIFV III
301 LMCSFHTYAA RVIPGSAAVY FCLVVLITML SAYYFDPRL L WDKRASDGIA
351 FNETEKYD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

m153.seq

```

1 ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC
51 GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CGGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTCCGC CTGTCACTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGCGGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGCGCGAA AAGTCTGAGT ATTTCTGCGG CGTTTCTGAC GGCGGCGGTT
601 ATTTTGTATT TCCCTGCCAA TATCCTGCCG ATTATGATTT CGTCCAATCC
651 TGCCCGCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCC
801 CTTCGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTTT GACGATGCTG TCCGCCTATT
1001 ATTTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

m153.pep

```

1 MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51 VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY

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438

```

101 IKLSSVAEVR FGPAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSLs ISSAFLTAAV
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHYYAA RVIPGSAAVY FCLVVILTML SAYYFDPRLW WDKRASDGIA
351 FNETEKHD*

```

m153 / g153 96.1% identity in 358 aa overlap

```

              10      20      30      40      50      60
m153.pep    MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEVMFVLTFGAPVLFLLCLYV
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g153        MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEVMFVLTFGAPVLFLLCLYV
              10      20      30      40      50      60

              70      80      90     100     110     120
m153.pep    YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g153        YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAKVRFGPAFYLMFA
              70      80      90     100     110     120

              130     140     150     160     170     180
m153.pep    LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g153        LSVMLIRTSVSVSPQHWVYFQIGRLTGNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE
              130     140     150     160     170     180

              190     200     210     220     230     240
m153.pep    LYRRRPKSLsISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g153        LYGGRPKSLsISSAFLTAAVILYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI
              190     200     210     220     230     240

              250     260     270     280     290     300
m153.pep    AAVIFSASILVPVLKIAAMS VLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g153        AAVIFSASILVPVLKIAAMS VLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII
              250     260     270     280     290     300

              310     320     330     340     350     359
m153.pep    LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLW WDKRASDGIAFNETEKHD
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g153        LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLW WDKRASDGIAFNETEKYD
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

a153.seq

```

1   ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACCTT CGGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTCGC TTCGATCGG CGTTTATCT
351 GATGTTTCGC CTGTCGGTTA TGCTGATTTC GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CCGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCTGCGG CGTTTCTGAC GCGGCGGTT
601 ATTTGTATT TCCCTGCCAA TATCCTGCCG ATTATGATTT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTCCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG
801 CTTGCTTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA

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439

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851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
  1 MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
 51 VLFLLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VEFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL SISAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHYYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGI
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
a153	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
  1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
 51 CAAAAACAAC accttctct CCGCGTCTG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCG CGGCTGGCTT TGGGTAAAG AAATCCGCA CAGGGGCGCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCATTAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

```

401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcccG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACACAGG CAGCGGCATC AAACCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCCT GTcgaATACA AAGGGCtgaA
951 TGTcggCATG GTTTCGGATG TCCCTTATTT TGACCGCAAt gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAAACAACA
1101 ATTCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCAAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTTCG
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGTCCATT GacaAACTGG TCGgcaatCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGAgacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAAaagacg TtcaACCCGT CATTAACTT TTGaaAGAAa
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAAGacc tatCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

g154.pep

```

1 MTDNSPPPNQ HAQARVRKNN TFLSAVVLVP LIALIAGGWL WVKEIRNRGP
51 VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTL LSGSYIAFTPG KSGEAKDVFQ
151 VQDIPPVTAI QSGSLRLNLI GKNDRIILNVN SPVLVENFMV GQIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGATSFDSF KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVaelN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQTL KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

m154.seq

```

1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51 CAAAAACAAC ACCTTCCTCT CTGCCGCTCT GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTATCAAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACACAGG CAGCGGCATC AAACCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCGGCG CGATTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTCGCCC GTCGAGTACA AAGGGCTGAA
951 TGTCCGGCTG GTTTCGACG TCCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```

```

1201 TCACCTAAGC TGCAGCCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAACTT TTAAAAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

m154.pep

```

1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLMLDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFG
151 VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN SPVLYENFMV QVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINAEQSS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLMLDSAE					
g154	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLMLDSAE					
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFG VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN					
g154	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFG VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFMV QVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETGSGI					
g154	SPVLYENFMV QVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETGSGI					
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDRS LYYTAFKQ					
g154	KLNSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDRS LYYTAFKQ					
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINAEQSS					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINAEQSS					
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					

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	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDLQVKLADLLDKFDKLPDKTVAEI NGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
g154	GGLDDLQVKLADLLDKFNNLPDKTVAEI NGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVPVINTLKEKPNALIF					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
g154	NNSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154 . seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAACAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCCG TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCT GGAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTTATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTCGGCGTG GTTTCGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGA AAATGCCGA CGAACAAAGC AAAGAACATT GGAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGCG GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAAACTG CCTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAAGTGA CCAAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTAAGAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTQQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFDQ

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151 VQDIPPVTAI QSGRLRLNLI GKNDRIILNVN SPVLYENFMV QQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIAATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPGTQ NIPNELNQTQ KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*
```

m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPENGHAQARVRKNNTFLSAVWLVLIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
a154	MTDNSPPENGHAQARVRKNNTFLSAVWLVLIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
a154	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFQVDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
a154	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFQVDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
a154	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ					
a154	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ					
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIAATQG					
a154	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIAATQG					
	370	380	390	400	410	420
m154.pep	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPGTQ					
a154	GGLDDLQVKLADLLDKFDKPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPGTQ					
	430	440	450	460	470	480
m154.pep	490	500	510	520	530	540
	NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540

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```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1   atGAAaatcg GtateCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGTCTA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGCGCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCCCGC ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGCG
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTGGTG ATTTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACCAAA GAAATGTTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTCCCGCCT CCGccgaTTc aggtTTCgc cggccgCAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagccc AgccGaaacc tgttCCctg
1201 tggaAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgcgtgGgt
1251 cggCgcggtc gcacccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCTGCGT CATCGGTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGAgtgcggt aaccaaCgcc atctccGGCA tcatggctgt
1401 cggCGCGCTG CTGCAAAATCG GTCAGGGcaa cggcttcgtT TCgctGCTGT
1451 CGTTTGTTGC CATCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1   MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTI V SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTNGVKII GYTDMANRLA GQSSQLYATN LVNLTkLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPP PPIQVSARPO QTPSEKAAPA AKPEPKVPPL
401 WKKLAPAAIA AVLVLWVGAV APAaFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIGQGNFV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMFK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1   ATGAAAATCG GTATCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTGCAAAAG CGGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAAGT CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

```

301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GGCGGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAATATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGAAAAA AACTCGCGCC CGCCGTCATC GCCGCCGCT TGGTACTGTG
1251 GGTGCGGCGC GTCGCACCCG CAGCATTCTT GAACCACTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCTG ATTGCCGCA TCAACATCT CGGCGGCTTT
1501 GCGGTAAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPV ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTQGITA A GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAAP GKPAKPLTK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YYVWNVVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155           MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep      AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPV
              |||:|||||
g155           AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPV
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep      ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155           ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA

```

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	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFAEQAKEVDIIITTAaipgkPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAaipgkPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPPIQVSAQPQPTSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
	: : : :					
g155	VTRDGEITFPPPIQVSARPQPTSEKAAPAAKPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
	360	370	380	390	400	410
	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAAATCG GTATCCCACG TGAGTCATTA TCCGCGGAAA CCCGCGTCCG
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTGCAAG CGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGCTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCGTG GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTCGCGCG CGCAGGCTTT GGACGNTTTG TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGCGCAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GGCGACGGGC GGCAACTGCG AACTACCAA ACAGGGCGAA
901 TTGTTTCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTAAAGC CCGAACAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CTTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCCAAGC CCGAACCAGG ACCCGTTCCC

```

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1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGGGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTCTTCG
1301 TCCTGCGCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTGTTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAaip GKPAPKXXXK EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPSEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YYVWNVVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQGNGF VSLLSFVAIL IASINIFGGF
501 FVTRRMLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

m155.pep	10	20	30	40	50	60
	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
m155.pep	70	80	90	100	110	120
	AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
	70	80	90	100	110	120
m155.pep	130	140	150	160	170	180
	ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQGITAAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTQGITAAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFFQESGSGGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDFFQESGSGGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAaipGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLFAEQAKEVDIIITTAaipGKPAPKXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPIQVSAQPQQTPSEKAVPAKPEPKVPPLWKKLAPAVIAAVLVLVWGA					
a155	VTRDGEITFPPIQVSAQPQQTPSEKAAPAAKPEPKVPPLWKKLAPAXIAAVLVLVWGA					
	370	380	390	400	410	420

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```

              430      440      450      460      470      480
m155.pep      VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNF
              |||||
a155           VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNF
              430      440      450      460      470      480

              490      500      510
m155.pep      VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX
              |||||:||||| |||||:|||
a155           VSLLSFVAILIASINIFGGFFVTRMLNMFRKGX
              490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CAGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTCG
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51 HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGGTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CAGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251 CGCTTGCCTG CCTGTTTCATC CTGTTCCGCC TCGCCTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTCG
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51 HAAQONGFEA FAPFAAAVLT AHATGNAAQS TINTLACLF LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m156 / g156 96.1% identity in 127 aa overlap

              10      20      30      40      50      60
m156.pep      MTFAYWCILIACLPLFCAAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              |||||
g156           MTFAYWCILIACLPLFCAAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep      FAPFAAAVLTAAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV
              |||||:||||| |||||:||||| |||||:||||| |||||:|||||

```

449

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
  1  ATGACTTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAA AAGCGGGCGG ATTCCGTTT AAAGACAACC
101  ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201  CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251  CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301  ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351  CTGCACCGTC GGGCTGTTT TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
  1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
 51  HAAQONGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LRLAFIWCY
101  IADKAALRSL MWVGGFVCTV GLFVVAAX*

m156/a156  90.6% identity in 127 aa overlap

              10      20      30      40      50      60
m156.pep    MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAARAHAQONGFEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a156        MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAQONGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep    FAPFAAAVLTAHATGNAAQSTINTLACLFILRLAFIWCYIADKAAMRSLMWAGGFACTV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a156        FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGFVCTV
              70      80      90      100     110     120

m156.pep    GLFVAAAX
           ||||:||||
a156        GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
  1  atgaggaacg aggAAAAACg cgccctgcgc cgcgaaattgC gCgGgcggcg
 51  ttcgcAAATg GGgcgagacg tGCGgGCGC GGCGgCgatA Aaaatcaacc
101  gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151  cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTtgtcCGCG CGGCGCAAAA
201  ACGCgCGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGCGGGA
251  TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301  GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351  GCACGGTTTG TCGGTATTGC TCGTCCCCTG TGTCGGCATA GACCGCGAAG
401  GCTACCGTTT GGGGCAGGCA GGCGGCTATT ACGATGCGAC GCTTTCGGCG
451  ATGAAATACC GTTTGCAGGC GAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501  GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551  TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
 51 PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMRERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
 51 TTCGCAAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAATCGG CGTGATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCCGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GGCGGCTATT ACATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTCAGGCA AAAAACCCTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGACGGTT
551 TTGTGTCGGA GGCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
 51 PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
101 GRAKLHVPQF AGRKKRVHDL NLLVPPVVG DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m157 / g157 88.1% identity in 193 aa overlap

      10      20      30      40      50      60
m157.pep MRNEEKRALRRELRGRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g157      MRNEEKRALRRELRGRRSQMGRDVRAAAAIKINRLLKRYIKRGRKIGVYWPMGKELRLGG
      10      20      30      40      50      60

      70      80      90     100     110     120
m157.pep FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKKRVHDL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g157      FVRAAQKRGAKLYLPYIEPHTRMWFTYPERGMERERKRGRAKLHVPQFAGRKIRVHGL
      70      80      90     100     110     120

      130     140     150     160     170     180
m157.pep NLLVPPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g157      SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP
      130     140     150     160     170     180

      190
m157.pep LDGFVSEAGILCFX
|||||:|||||
g157      LDGFVSEAGILCFX
      190
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCCG
 51 CGCGCAGATG GGCATCAAG GGCGGTTGGC GGCGGGGCAA ACGATTAAAC
```


451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCCGCT TCGCGGCCGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATAACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTGCGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

a157.pep

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRG A KLYLPYIEPR SRRMWFTYP ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLQA GGYDATLAA
151 MKYRLQAKTV GVGFAQFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLLKRYIKRGRKIGVYWPMGKELRLDG					
a157	MRNEEKHALRRELRRARAQM GHQGRLAAGQTINRLLKRYIKRGRKIGVYWPMGKELRLDG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAEALYLPYIEPRSRMWFTYPADGVKQERKRGRKALHVPQFAGRKKRVHDL					
a157	FVRAAQKRGAKLYLPYIEPRSRMWFTYPESGMRERIRGRAKLNVPQFAGRKIRVHGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLLVFVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
a157	SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL					
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

g158.seq

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGCTc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTGCGCGT GGATTCGCGG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCTT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

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801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
 851 TATTTTTGGA TTTTATTAGT AAGGAACTGG GAAAAAATAT GAATAGAACG
 901 AATACCAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep
 1 MKTNSEELTV FVQVVEGSGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFERR QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR
 301 NTK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
 151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATTCCGCG
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
 351 ACGCTATCCG CATATCCGAC TTTCTGCTCGT TTCTTCCGAA GGCTATATCA
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCCGG AGAATTGGAC
 451 GATTCCGGGC TCGGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
 601 ACATGGGCGG TTTTAGATGC GCAGGAAAT CCCTATAAGA TTTACCCGCA
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGTT
 701 GCGGTATTGT TTGCTTATCA GATTTTGGG TTGACAACGA CATCGCTGAA
 751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
 851 TATTTTTGGA TTTTATTAGT GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep
 1 MKTNSEELTV FVQVVEGSGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFERR QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSGSF	SRAAEQLAMANS	AVSRIVKR	LEEKLGVNLL	NRTTRQLSLT	
g158	MKTNSEELTVFVQVVEGSGSF	SRAAEQLEMAN	AVSRIVKR	LEEKLGVNLL	NRTTRQLNLT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRQRILQEMAAA	ETEMLA	VEI	PQGVLSVDS	SAMPMVLHLLAP	LAAKFNERYP
g158	EEGAQYFRRQRILQEMAAA	ETEMLA	VEVPQGVLRVDS	SAMPMVLHLLAP	LAAKFNERYP	
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	: : : : :					
g158	HIRLSLVSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
	: : : : : : : :					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	: : : : :					
g158	DFLVDNDITEGKLIPLFAEQTSNKTTHPFNAVYYSDKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTC AAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATCCCGGCG	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTTGA	TTTTTTAGTG	GAGGAACCTG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRA	QRILQEMAAA	ETEM LAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQ	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYSDKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANS AVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	: : : : :					
a158	MKTNSEELTVFVQVVESGSFSRAAEQLAMANS AVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRAQRILQEMAAAE TEM LAVHEIPQGVLSVDSAMP MVLHLLAPLA AKFNERYP					
	: : : : :					
a158	EEGAQYFRRAQRILQEMAAAE TEM LAVHEIPQGVLRVDSAMP MVLHLLAPLA AKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSNKTTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCCgcGTCC  GGTcGGCACG  GGCGATATTG  TATTTTTCCC
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTTG  ATGAACGGGC  TGCCGAAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACCTT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTcGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGcACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAC  CCCGATTTCG  GTTTTGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTCGG  CAAGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVVN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAEAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKKTPTS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTCGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTGCTC

```

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```

501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTCCGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
  51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
 101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
 151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
 201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
 251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
 301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      MDILDKLV DLAQLTGSADVQ CLLGGQW---HETLQREGLV HIVTAGSGYL CIDGETSPRP
          10      20      30      40      50

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      VGTGDIVFFP RGLGHVLSHD GKYGESLQPD IRQNGTFMVKQCGNGLDMSL FCARFRYDTH
          60      70      80      90      100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SEKPLTGTVS VVNALPSVLL VLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNI DKMVA AANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      PHAFVNHIRL QKGALLLKN PDSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
  1 ATGGACATTC TGGACAAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
 51 GGATGTGACAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

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```

101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCC GTTTCGGCTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90     100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90     100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          |||||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||||
a160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||
a160      PHAFVNHIRL QKGALLLKKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GGCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 CCGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GGCGTGCGCA TGTCGTCggt ttgggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tgggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTTTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVVLL LNPFSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATT A TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GGCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCTCGC TTTCTTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTTCTG GGCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RDXERTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVVLL LNPFSFRSGQE

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458

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151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

```

          10      20      30      40      50      60
m161.pep MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRM LFSTVALGAAAVL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g161      MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRM LFSTVTLGAAAVL
          10      20      30      40      50      60

          70      80      90     100     110     120
m161.pep RRDXFRTPHWKNHLNRSMTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g161      RRDTFRTPHWKNHLNRSMTGAMLLLFYAVTHLPLTTGVTLSTSSIFLAVFSFLILKE
          70      80      90     100     110     120

          130     140     150     160     170     180
m161.pep RISVYTQAVLLLG FAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVREL SLAGEPG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g161      RISVYTQAVLLLG FAGVLLLNPSFRSGQEP AALAGLAGGAMSGWAYLKVREL SLAGEPG
          130     140     150     160     170     180

          190     200     210     220     230     240
m161.pep WRVVFYLSVTGVAMSSVWATLTGWHTLSFP SAVYLSGIGVSALIAQLSMTRAYKVGDKFT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g161      WRVVFYLSATGVAMSSVWATLTGWHTLSFP SAVYLSGIGVSALIAQLSMTRAYKVGDKFT
          190     200     210     220     230     240

          250     260     270     280     290     300
m161.pep VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g161      VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR
          250     260     270     280     290     300

m161.pep X
          |
g161      X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

```

a161.seq
1   ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTC A
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCCGCAC
201 GCGCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCTGAT
351 TTTGAAAGAA CGGATTTCCG TTACACGCA GCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCGCGAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGCGGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACC CGGC TGCGCGCTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCATCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTCTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTTCTG GCCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA

```


851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLES
51 TVALGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSCIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLES					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSCIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSCIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
	I					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTt
151 ctgGGTTTTc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGCTTA TTTGGTTTC

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451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCCTTGGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACCTAC CTCGGAATC
851 TGGTGCGCCT CAGTTTGAAG ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAAACG CTGCTTTTAA
1151 AATTCCTTAA TTACCTCCCC CTGCCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTATATG
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGCTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1  MVILTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLEFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFSWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITSRDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1  ATGGTTATTT TGACGACTTT GTTTTTTGTTG TGTGTTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTTAC CGAGTTCAGC TGTTTTTATG TTTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGCCGGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCTG GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCCTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGGCGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGAGGAG CAGGATATTT TAAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFWSTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVQDQVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQQL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

```

m163.pep      10      20      30      40      50      60
               MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFSWFWYVLTFSIFLGFLILSVS
               |||||
g163           10      20      30      40      50      60
               MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFSWFWYVLTFSIFLGFLILSVS

m163.pep      70      80      90     100     110     120
               SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
               :|||:|||||
g163           70      80      90     100     110     120
               GLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ

               130      140      150      160      170      180

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m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFGVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRSLFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVRIMSQTQEODILKFLKHTASPAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC  CGAGTTCAGC TGTTTTATG  TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACACT CTCGGAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCTGTT CGGCGTTTTC
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACTTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTAGCCTG TGAAAGGAT
1451 TGAGTCCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACACCGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAGTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

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This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

a163.pep

```

1  MVILTTLFFV CVLVVLVLT VPQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFWYVLTFISIFLGFLILSVS
          |||||
a163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFWYVLTFISIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQ

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|||||
a163      SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
          70      80      90      100     110     120

          130     140     150     160     170     180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
          130     140     150     160     170     180
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
          130     140     150     160     170     180

          190     200     210     220     230     240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAMVSLAVVSAISGVGK
          190     200     210     220     230     240
a163      MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAMVSLAVVSAISGVGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m163.pep  GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
          250     260     270     280     290     300
a163      GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
          250     260     270     280     290     300

          310     320     330     340     350     360
m163.pep  WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
          310     320     330     340     350     360
a163      WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
          310     320     330     340     350     360

          370     380     390     400     410     420
m163.pep  WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
          370     380     390     400     410     420
a163      WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
          370     380     390     400     410     420

          430     440     450     460     470     480
m163.pep  ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
          430     440     450     460     470     480
a163      ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
          430     440     450     460     470     480

          490     500     510     520     530     540
m163.pep  WKGLSADKKYFETRVNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKQTAS PAMHELQR
          490     500     510     520     530     540
a163      WKGLSADKKYFETRVNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKHTAS PAMHELQR
          490     500     510     520     530     540

          550     560     570     580     590     600
m163.pep  ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
          550     560     570     580     590     600
a163      ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
          550     560     570     580     590     600

          610     620     630     640     650     660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGELMAHEQVELAE
          610     620     630     640     650     660
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGELMAHEQVELAE
          610     620     630     640     650     660

m163.pep  X
          |
a163      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCTGTTCG CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCC GTCGAAAAAA TCATTTGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCCG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTAT CGTTTTcctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCCCCGAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGGCGA AGTGGGCGAA CTGATCGTCA
851 GGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCGATTTCC TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCGTCATC GCGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTTGG
1151 GCGAGGACGA aatccgccgc caccTGCCTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPD LGQRPR INDLAHIIT SGTTHGPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVDIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPEATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKKD LIISKQONVY PREIEEIEHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCTGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTAT TACCGCTATT TCGCCATCTC CGCCATCGGC GCGTTCGCCG
251 TACCGATGAA CACATTTTTG AAAAAACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGACCGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGATATAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCCAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTGG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTT AGATGTTTCA
851 ACCGCATTCG CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACCTGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRD R FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNV L
251 KQTLKRA TV FLGVP AIYTA MSKAKIPWYF RWFNRIRLF I SGGAPLAEQT
301 ILDFKAKFP R AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLMN PAATDETIVN GWLKTGDFVT
401 IDEDGFI FIV DRKKDLISK QONVYPREIE EEIYKLD AVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRV LK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

m164.pep      60      70      80      90      100      110
GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
g164          10      20      30
MNTFLKNSEYAYILNDCKARFLFASAGLSK

m164.pep      120      130      140      150      160      170
ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
g164          40      50      60      70      80      90
ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT

m164.pep      180      190      200      210      220      230
SGTTGHPKGALISYANL FANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC
g164          100      110      120      130      140      150
SGTTGHPKGALISYANL FANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC

m164.pep      240      250      260      270      280      290
SIILVKSVPF PFSNV LKQTLKRA TVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP
g164          160      170      180      190      200      210
SIILVKSVPF PFSNV LKQALLKRA TVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP

m164.pep      300      310      320      330      340      350
LAEQTILDFKAKFPRAK LLEGYGLSEASPVVAVNT PERQKARSVGIPLPGLEAKAVDEEL
g164          220      230      240      250      260      270
LAEQTILDFKAKFPRAK LLEGYGLSEASPVVAVNT PERQKARSVGIPLPGLEAKAVDEEL

m164.pep      360      370      380      390      400      410

```


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```

m164.pep  VEVPRGEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          |||||
g164      VEVPRGEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKGQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          |||||:|||||
g164      LIISKGQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          |||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCTGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGT AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTTGAGAC
451 GTGCGCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGATAAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTCGGCTAAT CAGCTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTTG
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAACCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACCTGA TGCCGTCGAA GCCGCGCCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTGAAG GAGCAGTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKFDL GRQPRINDLA HIIYTS GTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPAIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLISK QONVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA

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468

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIGVKFGDTVA					
a164	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIGVKFGDTVA					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
a164	KAQTPVEKIIWTDKSRPDGEMAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKTRATVFLGVPAYITAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFPFSNVLKQALLKTRATVFLGVPAYITAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSGVIGPLPGLEAKAVDEELVEVPR					
a164	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSGVIGPLPGLEVAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFVDRKKDLIISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFVDRKKDLIISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCCTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTT CCTCGGCGCG GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTCG GTCCTTACGC
951 AGGTTTCCGT TCCAATTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CcTGCTGGgC gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFER NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGYAGER SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCCTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGCA CGGGGCATTC CGCGCTGTG GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

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470

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201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEQH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTK...

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

```

              10      20      30      40      50      60
m165.pep    MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
              |||||||
g165         MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
              10      20      30      40      50      60

              70      80      90     100     110     120
m165.pep    ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              |||||:|:|:|
g165         ELNYAPLGADGVINPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              70      80      90     100     110     120

              130     140     150     160     170     180
m165.pep    HCSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF
              || |||||:|
g165         HCRYLQKRYDVFKTQKLFENMEFSTDNRNKISDWAPLIMRGRDENQPVAANYSAEGTDVDF
              130     140     150     160     170     180

              190     200     210     220     230     240
m165.pep    GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA
              |||||||
g165         GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDWQLTLRTRFLFLGA
              190     200     210     220     230     240

              250     260     270     280     290     300
m165.pep    GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNKAVYQASVGAPPMSPVPHL
              |||||||
g165         GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEQHNKAVYQASVGAPPMSPVPHL
              250     260     270     280     290     300

              310     320     330     340     350
m165.pep    DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMLDLPLSIHMDNLYPMLCAGWANMPLTK
              |||||||
g165         DTRNVDGKRHLMFPGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
              310     320     330     340     350     360

g165         ELRX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

```

a165.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGCGA AGGCGGTAAA AACCGAGTTC

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471

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCGC CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCATTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYGQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA QORVQIIKKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

```

          10      20      30      40      50      60
m165.pep MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWN NAGTGHSALC
          |||
a165      MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWN NAGTGHSALC
          10      20      30      40      50      60

          70      80      90     100     110     120
m165.pep ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
          |||
a165      ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
          70      80      90     100     110     120

          130     140     150     160     170     180
m165.pep HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDF
          |||
a165      HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDF
          130     140     150     160     170     180

          190     200     210     220     230     240
m165.pep GRLTRQMVKYLQKGKVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
          |||
a165      GRLTRQMVKYLQKGKVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
          190     200     210     220     230     240

          250     260     270     280     290     300
m165.pep GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSVPHL
          |||
a165      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSVPHL
          250     260     270     280     290     300

```

472

	310	320	330	340	350
m165.pep	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG				
	310	320	330	340	350
					360
a165	ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS				
	370	380	390	400	410
					420

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAAGat  gTGGCGTTGG  AATCGTCAAA  cGCGTGGAAC
151 AACGcCGgca  CGGGGCATTC  CGcGCTGTGc  GAATTGAACT  AtgcgcgGCT
201 GGGtgcgga  ggcgtcatCA  ATCCGGCGCg  cgCCCTGAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGcga  cgctggTCGC  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTGAT
351 GAACGAAGAC  CACTGCCGTT  ACCTGCAAAA  ACGCTATGAT  GTGTTAAAA
401 CGCAGAACT  TTTTGAAAAT  ATGGAATTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CtcgcGTGAT  TATGCGCGGC  CGGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TATTCGCCG  AAGGCACGGA  TGTCGATTTC  GGACGGCTGA
551 CGCGCCAGAT  GGTGAAATAT  TTGCAGGCA  AGGGCGTAAA  AACCAGATTTC
601 AACC GCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCAGACTG  GCAGCTCACC  CTCGCGACCC
701 GCTTCTCTTT  CCTCGGCGCG  GCGGCGGCG  CACTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTACCCG  TGTCCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAACAC  AACGCCAAAG
851 TGTACGGGCA  GGCTTCCGTC  GCGCGCGCG  CGATGTCCGT  CCCGCACCTC
901 GACACACGCA  ACGTAGACGG  CAAACGACAC  CTTATGTTTC  GTCCTTACGC
951 AGGTTTCCGT  TCCAACCTTC  TCAAGCAAGG  CTCGTTTATG  GATTGCGCGC
1001 TGTCCATCCA  TATGGACAAC  CTCTATCCTA  TGCTGCGCGC  CGGCTGGGCG
1051 AATATGCCGC  TGACCAATA  CCTGCTGGGC  GAATTGCGTA  AAACCAAGA
1101 AGAATGCTtt  gCCTCCCTGC  TGgaatacta  cccGaggcag  acccGACGAc
1151 tgg tactcat  cagcgagcnc  acGCGTcata  tcattanata  tgactCgaaa
1201 ctgcgcgtgc  tgcagttgta  cgagattgtg  ccaCGCGacg  ctcgctcgcg
1251 cattctggag  cgtcgcggcg  catcacgctn  tgcgctgata  tccgctgatg
1301 acactgctcc  gaGCGcgccc  gtcttgga  gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSALE  ELNYAPLGAD  GVINPARALN  IAEQFHVSRO  FWATLVAEGK
101 LEDNSFINAV  PHMSLMVNED  HCRYLQKRYD  VFKTQKLFEN  MEFSTDRNKI
151 SDWAPLIMRG  RDENQPVAA  YSAEGTDVDF  GRLTRQVMKY  LQKGKVKTEF
201 NRHVEDIKRE  SDGAWVLKTA  DTRNPDWQLT  LRTRFLFLGA  GGGALTLLQK
251 SGIPEKGKYG  GLPVSGLFFR  NSNPETAEOH  NAKVYGOASV  GAPPMSPVPHL
301 DTRNVDGKRH  LMFPGPYAGFR  SNFLKQGSFM  DLPLSIHMDN  LYPMLRAGWA
351 NMPLTKYLLG  ELRKTKEERF  ASLLEYPRQ  TRRLVLITQX  TRHIIXYDSK
401 LRVLLQYIEIV  PRDARSRILE  RRGASRXALI  SADDTAPSAP  VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAAGAT  GTGGCGTTGG  AATCGTCAAA  CGCGTGGAAC
151 AACGCGCGCA  CGGGGCATTC  CGCGCTGTGC  GAATTGAACT  ATGCGCCGTT
201 GGGTGCAAA  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGCTGGTCGC  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTGAT
351 GAATGAAGAC  CATTGTCTTT  ATCTTCAAAA  ACGTTATGAC  GCGTTAAAA
401 CCCAAAACT  TTTTGAAAAT  ATGGAATTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CTCCGCTGAT  GATGCGCGGC  CGGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TACTCCGCCG  AAGGTACGGA  TGTCGATTTC  GGACGGCTGA
551 CGCGCCAAAT  GGTGAAATAT  TTGCAGGCA  AGGGCGTAAA  AACCAGATTTC
601 AACC GCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCGACGCG  GCAGCTCACC  CTCGCTACCC
701 GCTTCTCTTT  CCTCGGCGCG  GCGGCGGCG  CGCTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTCCCG  TGTCCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAACAC  AACGCCAAAG

```

```

851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCGAGGCA AACCCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALE ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

m165-1.pep	10	20	30	40	50	60
g165-1	10	20	30	40	50	60
m165-1.pep	70	80	90	100	110	120
g165-1	70	80	90	100	110	120
m165-1.pep	130	140	150	160	170	180
g165-1	130	140	150	160	170	180
m165-1.pep	190	200	210	220	230	240
g165-1	190	200	210	220	230	240
m165-1.pep	250	260	270	280	290	300
g165-1	250	260	270	280	290	300
m165-1.pep	310	320	330	340	350	360
g165-1	310	320	330	340	350	360
m165-1.pep	370	380	390	400	410	420
g165-1	370	380	390	400	410	420
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
:
g165-1 ILERRGASRXALISADDTAPSAPVLESVX
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTCT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAAT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTT CCTCGGCGCG GCGCGCGCGC CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACCTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTGTGGA TATTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLLTRQVMKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQGASV GAPPMSVPHL
301 DTRNVGDKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPLMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKKD
401 SEKGVVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
m165-1	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMMRGRDNQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMMRGRDNQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240


```

a165-1.pep  GRLTRQMVKYLGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1      GRLTRQMVKYLGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
|||||
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
|||||
m165-1      YTAKVLDIX

```

a165-1/p33940

```

sp|P33940|YOJH_ECOLI_HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF_ID:o372#5; similar to [SwissProt Accession Number
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct
identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

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```

Query: 3  EATDVVLVGGGIMSATLGVLKLEEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63  NYAPLGGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSGISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122  CSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150  VNFLRARYAALQQSSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQKVAATRTEIGTDVNYG 209

Query: 182  RLTRQMVKYLGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210  EITRQLIASLQKKSNSFLQLSSEVRALKRNDNTWTVTVADLKNGTAG-NIRAKFVFIGA 268

Query: 241  XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269  GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329  DTRVLDGKRVLFGPFATFSTKFLKNGSLWDLMSSTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389  QVMLSEEDRFELKEEYYPQAKKEDRWLWQAGQRVQIIKRDAEKGGVLRGLGTEVVSDDQQT 448

Query: 421  XXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

```

476

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508
 Query: 479 IAYTAKVLDI 488
 + YT++VL +
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcggcgg cggaaataaa acgccccctc gctgtcgatt tccagcacat
 51 agcgtccgtt ctgcacggcg gcatagccgc ttttgccctgc ctgataggg
 101 tgcaggcggc aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
 151 ggcgatattg cccaccagtt tggcaaaaca ggtatggcac acgccgtttt
 201 ccgcccagcc cgaaggcggc tcctttccgt cggtttccat acatttgccg
 251 acgacggctt ccaagtcgtt gggatgctt ccggtcagcc ggacggcgtt
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcgc tttgtgccgc
 451 attttgcggc tgttccgccc tattttcggg tttgccgcag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc
 701 ctgcctgcaa aatctcttcg atttgcgaag gattagaggt caatgcgttg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQVV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDFD ENRFRRALCR
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKCRLLKRGR
 201 RFGRHVVYFN GRMPTASRTL SNNRASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTGTCCG
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTTGTTTT TTGCCGTCTG
 351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
 451 GTTTTGCGGC TGTACCGCCG TATTTwCGGA TTTGCCGCaC GGCaArGCAG
 501 CAGGCAGCGG CCAATACGG CAAAaArAwGT wTTCAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
 651 ATAATTCGCG TGCTTCTTTA CGCGCTTTTC CCGCGCCTGC CTGCAAAATC
 701 TCTTCGATTT GCGAAGGGTC GGCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR
 151 VLRLYRRIxG FAATAXQQA AYGKXXXQH STXLMVSKCR LKRGRRRFGR
 201 HRVHFNGRMP TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

m204/g204

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204.pep

1	MAAAEIKRPL	AVDFQHIASV	<u>LHGGIAAFAC</u>	<u>LIGLQGGMRN</u>	QVIRQFAAVF
51	GDIAHQFGKQ	GMAHAVCRPA	RRRALS V GFH	TFADDGFQVV	GMLAQGPDDV
101	LFRQAF....
151KRFRGR
201	HWVYFNGRIP	TASRTLPNNS	RASLRAFCAP	ACKISSICEG	SAVSSI*

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLQGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRTDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVGFHTFADDGFQVVGMLAGQPDVLFQRAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTNRRIVDIYDFENRFRRALYRVLRLYRRIXGFAATAXQQAAYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKRRRFRGRHVFHNGRMPTASGTLNNSRASLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNSRASLRAFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcctgccgc
51  ctgcgcgcaaa tccgaaaaata cggcgggaaca gccgcaaaat gcggcacaaa
101 ggcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgcttcg ggctgggcgg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caataticgc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggtatgc cgccgtgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccgcat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNI A EDGKLT DYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAAwA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CGGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTTGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAACTGACG GATTACCTAG TTTCGCATGC CGCCCTGCAA CCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTCCGC CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
  1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
 51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101  METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLTDLV VSHAALQPYQ
151  AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNAVQSAPKPVFKVIYIDNTAAGLDLGQSSE
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205      MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTAAGLALGQSSE
          10      20      30      40      50      60

      70      80      90     100     110     120
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPAAGWAENGVCHT
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205      GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          70      80      90     100     110     120

      130     140     150     160     170     180
m205.pep  LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205      LFAKLVGNIAEDGGKLTDLVISHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130     140     150     160     170     180

m205.pep  YX
          |
g205      Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
  1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
 51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101  ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151  TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC
201  GGATTACCTG ATTCGCATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251  GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301  GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
  1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
 51  LFAKLVGNIA EDGGKLTDLV ISHSALQPYQ AGKSGYAAVQ NGRYVLEIDS
101  EGAFYFRRRH Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90     100
m205.pep  KVIYIDNTAAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
a205      SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep  METDDKDSPAAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ
```

```

||||| |: |||| | |||| | |||| | |||| | |||| | |||| | : ||| | |||| | |||| 
a205 METDGKGAPSGWAANGVCHTLFAKLVGNIAEDGGKLTDYLIISHSALQPYQAGKSGYAAVQ
           40         50         60         70         80        90

          170       180
m205.pep NGRYVLEIDSEGAFYFRRRHXYX
||||| |
a205     NGRYVLEIDSEGAFYFRRRHXYX
            100      110
```

1	ATGCTGAAAA	TAcCTTTTGC	CGTGTGGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAAAT	CAAGCGGACA	CGCCGCAAAAT	CGCGCACAAAA
101	GCGCGCCGAA	ACCGGTTTTC	AAAGTCAAAT	ACATCGACAA	TACGGCGGATT
151	CGCGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAAGGCTT	GCCGGAACAA	AACGCGCGTCC
251	GGTGACCCG	AAAGCATCCC	AACGACTTTG	AAGCCGTCGT	CGGCAAAATGT
301	ATGGAACAAC	ACGGAAGGGA	CGCGCCTTCG	GGCTGGGGCG	AAAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	TGATTACCTG	ATTTGCGATT	CCGCCCTGCA	ACCTATACAG
451	GCAAGCAAAA	GCGGCTATGC	CGCCGTGCAG	AACGGAACGT	ATGTGCTGGA
501	AATCGACAGG	GAGGGGCGGT	TTTA		

1	<u>MLKIPFVAVLG</u>	<u>GCLLLAACGK</u>	SENTAEQPQN	AAQSAPKPVF	KVKYIDNTAI
51	AGLALQGSSE	GKTNDGKKQI	SYPIKGLPEQ	NAVRLTGKHP	NDLEAVVGKC
101	METDGDAPDS	GWAENGVCHT	LFALKLVGNIA	EDGGKLTDYL	ISHSALQPYQ
151	AKSGSYAAVQ	NGRYVLEIDS	EGAF		

1	ATGCTGAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGCGCAA	TCCGAAAATA	CGCGCGAACA	CGCGCAAAAC	CGCGGTACAA
101	GCGCGCCGAA	ACCGGTTTTT	AAAGTCAAAT	ATATCGACAA	TACCGCGATT
151	CGCGGTTTGG	ATTTGGGACA	AAGCAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAAGGCTT	GCCGCGAACA	AATGTTATCC
251	GACTGATCGG	CAAGCATCCC	GGCAGCTTGG	AAGCCGTCAG	CGGCAAAATG
301	ATGGAACCG	ATGATAAGGA	CAGTCCGGCA	GGTTGGGCAG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACGTAC	GGATTACCTA	GTTCGTCATG	CCGCGCTGCA	ACCCATCGGA
451	CGAGGCAAAA	GCGGCTATGC	GGTTGCTGAC	AACGGACGCT	ATGTGCTGGA
501	AATCGACAGC	GAGGGGCGT	TTTATTTCGG	CCGCGCCCAT	TATTGA

1	MLKTSFAVLG	GCLLLAACGK	SENTAEQPQN	AVQSAPKPVF	KVKYIDNTAI
51	AGLDLGQSSE	GKTNDGKKQI	SYPIKGLPEQ	NVIRLIGKHP	GDLEAVSGKC
101	METDDKDSAP	GWAENGVCHT	LFALKLVGNIA	EDGKGLTDYL	VSHAALQPYQ
151	AGKSGYAAVQ	NGRYVLEIDS	EGAFVYRRRH	Y*	

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAQAQSA	PKPVFKVKYIDNTA	IAAGLALGQSSE			
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPQNAVQSA	PKPVFKVKYIDNTA	IAAGLDLGQSSE			
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAV	VGKCMETDGKDAPSGWAENG	VCHT			
m205-1	GKTNDGKKOISYPIKGLPEQNVIRLIGKHPGDLEAV	SGKCMETDDKDS	PAGWAENG	VCHT		

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```

              70      80      90      100      110      120
              130      140      150      160      170
g205-1.pep    LFAKLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m205-1        LFAKLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
              130      140      150      160      170      180
m205-1        YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1   CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TTCGGGCTGG GCGGCAACG GCGTGTGCCA TACCTTGTTT
151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGGCAAC TGACGGATTA
201 CCTGATTTCC CATTCGCCCC TGCAACCTTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCCGT GCAGAACGGA CGTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTTATT TCCGCCGCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1   PLKGLPEQNV VRLTGKHPND LEAVVGKCM ETDGKGAPSGW AANGVCHTLF
51  AKLVGNIAED GGKLT DYLVSHSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep    KYIDNTAIAGLDLGQSSEKTN DNGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCM E
              |||||:|||||:|||||:|||||:|||||:|||||
a205-1        PLKGLPEQNVVRLTGKHPNDLEAVVGKCM E
              10      20      30
              110      120      130      140      150      160
m205-1.pep    TDDKDSPAGWAENGVCHTLF A KLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNG
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a205-1        TDGKGAPSGWAENGVCHTLF A KLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNG
              40      50      60      70      80      90
              170      180
m205-1.pep    RYVLEIDSEGAFYFRRRHYX
              |||||:|||||:|||||:|||||:|||||
a205-1        RYVLEIDSEGAFYFRRRHYX
              100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1   atgttttccc ccgacaaaac ccttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atcccgcaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaa tcatccatgc ccccggcagc
451 ggcaaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttggg gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1   MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

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51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
 101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

m206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCGGAcA GCCGcYTCAA
 351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC
 451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep.
 1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
 101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPFYAKNYLGAHTFFTE					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCCTTAA
 351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC
 451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA

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This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
51  tgctgcgggt gatgtgccac tgctggcgca tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggtttgg gcgaaacatc ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgcccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 tgctgcggcg tatttttctt tgatggctcg cagttcgggt gcggcggcac
501 gcattttcgc catcgaaagg taggaggcgt tggtaaatgg atacagtacg
551 gctttgacga tgatggtaaa aacgacgatt gccagcccc agttgccgat
601 aatgttggtc agttggttca ggagccagaa gaggcgcat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctggc gatgtttcgg
701 ataacggatg tggtttcgag accggcatac aggttgaccg ccattttcgg
751 ttttggtccc cgggttgagg tagcggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRQTAA QRVDLFLFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEPE ERRCEPVYFT VFVCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGgGCGTT GTTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGGT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

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301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTCGGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGCTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTGCGGAT GTATTCGGCC
951 TCGGATTGTC CGGATTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDL DLQQRQAAA QRVDFLVCVK LHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTVLVLSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

```

m209/g209
      10      20      30      40      50      60
m209.pep MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDG ENQRHDFHHFR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEEHDG ENQRHDFHHFR
          10      20      30      40      50      60

      70      80      90      100     110     120
m209.pep LHRVGRRRVQ ISLGEHRCRH NDGQDVVG VGAAEVGNPTQ PRC LAQFYGGE QCPIQSDG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      LHRVGRRRVQ IGLGEHRCRH NDGQDVVG VGAAEVGNP AQPRC LAQFYGGE QCPIQADEG
          70      80      90      100     110     120

      130     140     150     160     170     180
m209.pep DLQQRQAAA QRVDFLVCVK LHRLLLRHT VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      DLQQRQTA AQRVDFLV FEKLHHRLLR HTVVAVFFDGL QFGCGGTHFR HRTVGGVGQW
          130     140     150     160     170     180

      190     200     210     220     230     240
m209.pep IQYGFDDDGXNDNRPAPVADDVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTV VFCQLQVVG DVCNDGCGLR
          190     200     210     220     230     240

      250     260     270     280     290     299
m209.pep AGVEVDGGFGF-APFWMAAKG TLTVLVLSL LRLMSMLHS PAAQTLCLPL GWRIQVDMK
          :|:|:| | | | |
g209      TGIQVDRHFR FFWPPGWD SG
          250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CCACTTCGCC TTGGGCGCGT TGTTTTTCGA

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51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201 GCGGGTTCAG ATAGGTTTGG CCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCCAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451 GTCGTCGCGG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCACT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTTGTCGGC GATGTTTGCG
701 ATAACGGATG TGGTCTGTGG GCCGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGTGCTGTA
801 CAGCTTGTCG TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGGA TGTATTCGGC
951 CTCGGATTG CCGGATTG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQT GREEEHHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRHRAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQPK EGGGEPVYFA VVFGQLQVVG DVCNCGCLW AGVEVDGGFG
251 FAPFWIAAKG TLTVLVLSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

m209/a209 95.6% identity in 341 aa overlap

	10	20	30	40	50	60
m209.pep	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR					
a209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m209.pep	LHRVGRRRVQISLGEHRCRHNDGQDVVGVAEEVGNPTQPRCLAQFYGGEQCPIQSDG					
a209	LHRVGRRRVQISLGEHRCRHNDGQDVVGVAEEVGNPTQPRCLAQFYGGEQCPIQSDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m209.pep	DLQQRHRAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW					
a209	DLQQRHRAAAQRVDFLVCVKLHHGLLRHTVVAVFLFDGLQFGCGGTHFRHRTVRGVGQW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m209.pep	IQYGFDDDGXNDNRPAVADDVVQLVQEPGEGGEPVYFAVFGQLQVVGDVCDGCGLR					
a209	IQYGFDDDGXNDNRPAVADDVVQLVQKPEGGEPVYFAVFGQLQVVGDVCDGCGLR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m209.pep	AGVEVDGGFGFAPFWMAAKGTLTLVLVLSLRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGFGFAPFWIAAKGTLTLVLVLSLRLMSIRQSPAAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
	310	320	330	340		
m209.pep	CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX					

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```

|||||
a209  CSIMPSQPVGVLRMYASDLPDLASSKSEKLTFWKLP SGVX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1   atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atgggtcggc
51  ggtgggaaac ggggtcgata agtttgggcg tgggtgctgat aatcagggttg
101 agtttttggg aggaaacctg attgtagtcg gcgcgtccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgcgccgcc gtttttgtcc
251 tggtcgcgca ggaacagggt ttcatgatg ccggattcgg tgtcaaagg
301 ttcgacgaaa taaacctgct cggtgcgctt gcccaggtta ttgaactcgc
351 cggcttcac caaagacaat tcctgcttct gttcaaaat ttcggcatat
401 tcgcggtcgc gcagctctgc ccacggatc acccaaagct gcagacggc
451 aatcaggatg gcaaacggca cggcaaactg catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1   MLRIAAANQL GGRNGAAVGN GVDFKFRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGVKG
101 FDEINPAVAL AQVIELAGFH QROFLLLLQN FGIFAAALC PRYHPKLHDG
151 NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1   ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGTGAT AATCAGTTG
101 AGTTTTTGGG AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTG TCGTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTCGCCGCC GTTTTTGTCC
251 TGTTGCGCGA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAATG TTGAACTCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAACG GCAAACGGCA CGGCAAATG CATCACGGG CGTATCCATT
501 GTTCAATGC CAATCCGCA GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1   MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QROFLLLLQD FSVFAAAXLC PRYHPKLHDG
151 NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211

          10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNVDFEFGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211       MLRIAAANQLGGRNGAAVGNVDFKFRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          10      20      30      40      50      60

          70      80      90     100     110     120
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 731>:

This corresponds to the amino acid sequence <SEQ ID 732; ORF 211.a>:

m211/a211 99.4% identity in 174 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 733>:

g212.seq (partial)						
1	atggacaatc	tcgatatggga	cggcattccc	gacatccgca	cactcgacca	
51	aaccatccgc	aaacacgcac	accgcgtcaa	cctgattgtc	tgccctccccg	
101	ataatcagat	tcccgatttt	caaaccgcac	aagatgcttc	ggactcggaa	
151	tgccgtctga	agcaccggtt	ggatcaggca	accagtgcc	tccagttcga	
201	cagcatcaac	ctcatcgaac	acatcctgcc	cgatgtccgc	ttctggettg	
251	ttcccccttc	acgcacccgc	cgctcgacg	aaacattcca	ccacatttcc	
301	tggcagaccg	aagccatccc	gcaaaccgaa	agcaagtccg	acaaaccttc	
351	qtttgcaatt	ccacaatacat	ccqaacqaaa	aaaaccqaaa	cacgtcctcc	

```

401 tcatcgggtgc aggcattgcc ggcgcacgca cgcgccacgc cttagcatca
451 cacggcatttt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccggacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattggggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatacacgc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgctc
851 gcaccctcct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcatttt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagccctt
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacccggc tcacaccgct caccgccgtt tccgaacaac tgcgttgcgc
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgccca agcattggca caccctaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 LGHISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
251 EKXAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LH CYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCGCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCATTGTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GGCGCGGCAA CCGCCACGC CTTAGCATCA
451 CACGGCATT CCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAATTGTTG CTTGCCGGCT ACGGCTACAC CAAACGCCGT
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTCGTCC
851 GCACCTCTCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCTTG
901 ACCGACATT CCCACGACGG GGA AAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGC GTTGC GC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCTAGT CGGCGCACTC
1351 GCGGACATTG CCGCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAATACCGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGACTCGCCA CCGCCCCCAT CTGCGCCGCC

```

1501 GmCAwTGcAG CCCAAATCsT AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAL PQTSERQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNQKH QGHAAIRCDS PDHPLVLGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIIICLPDNQIPDFQTAQDASDAECRLKHLRDQA					
	: : : : :					
g212	MDNLVWDGIPDIRTLDQTIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRLKHLRDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAL					
	: : : : :					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRLHEHFHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	: : : : :					
g212	PQTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	: : : : :					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
	: : : : :					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
	: : : : :					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEEASNRQALAHLPALSESSE					

	:
g212	SEQLRCAVSGESYISPSWHGLHCYGASFI PNSSNTGWNEAEASNQALAHLPALAESL
	370 380 390 400 410 420
	430 440 450 460 470 480
m212.pep	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
g212	F

a212.seq

1	ATGGACAATC	TCGCATGGAA	CGGCATCCCC	GACATCCGCA	CACTCGACCA
51	AACCATCCGC	AAACACGCAC	ACCCGCTCA	CCTGATTGTC	TGCCCTCCCG
101	ATAATCAGAT	TCCCAATTTT	CAAACGGCAC	AAGATGCTTC	GGCAGCGGAA
151	TGCCGTCTGA	AGCACC GTT	GGATCAGGCA	ACCCAGTGCC	TCCAGTTCTGA
201	CAGCATCAAC	CTGATTGAAC	ACATCCTGCC	CGATGTCCGC	TTCTGGCTGG
251	TTCCCCCTTC	ACGCACCCGC	CGCCTGCACG	AACACTTCCA	CCACATTTCC
301	TGGCAGACCG	AAGCCATCCC	GCAAACCGAA	AGTAAGCCCG	ACAAACCTCG
351	GTTTGCACTT	CCACAACAT	CCGAACGGCA	AAACACGGAA	CACATCTCTG
401	TTATCGGAGC	GGGCATATCC	GGCGCGGCAA	CCGCCACGC	CTTAGCATCA
451	TACGGCATTT	CCGTTACCGT	ATTGGAAGCC	CGAAAAGCCG	CCCAAGCCGC
501	CAGCGGCAAC	CGCCAAGGCG	TGCTCTACGC	CAAATCTCTG	CCGCACGACA
551	CCGAACAAAC	CGAATGCTG	CTTGCCGGCT	AGGGCTACAC	CAACGCCTG
601	CTCGGACATA	TCTGCCCCGA	ATCCGAAACC	TGGGGCGGCA	ACCGCATCAT
651	CCACCTCAAT	TACAGCCGCA	CCGAACAACA	ACGCAATCAC	GAATTGGGTT
701	TGCAAAAACA	CCATAACCAC	CTCTACGCA	GCATCAGCA	GGCAGAAGCC
751	GAAAAAATCG	CCGGCATCCC	TCTGAACACG	CCCTACGCCG	AACCATTATG
801	CGGATGTGTT	TGGCAGTAGC	CGGTATGGCT	CAATCCTCCC	ACATTCTGTC
851	GCGCCCTCCT	CAGCCATCCG	CTCATTGGAC	TACACGAAGA	CACACCGTTA
901	ACCGACATTT	CCCACGACGG	GGAAAAGTGG	ATTGCAAGCA	CGCCAAACGG
951	CACATTTACC	GCCACACACA	TCATCTACTG	CACCGGTGCG	AACAGCCCCT
1001	ACCTACCCGA	AACCAACCCT	GCCACCCTG	CCCTCAGGCA	AATACGCGGA
1051	CAAACCGGCC	TCACACCGTC	CACCCCGTTT	TCCGAACAAC	TGCGTTGCGC
1101	CGTTTCAGGC	GAAAGCTACA	TCAGCCCGTC	GTGGCAGGGA	CTGCCTGCT
1151	ACGGCGCGAG	TTTTATTCCC	AACAGCAGCC	ATACCGGATG	GAACGAAGCC
1201	GAAGAAGCCT	CAAACCGCCA	AGCATTGGCA	CACCTTAACC	CCGCCCTTTC
1251	CGAATCATTG	TTTGCCGCCA	ACCCAAACCC	CCAAAAACAC	CAAGGGCACG
1301	CCGCCATACG	CTGCGACAGC	CCCGACCACC	TTCCCTTAGT	CGGCGCACTC
1351	GGCGACATTG	CCGCTATGCA	ACAAACTTAC	GCCAACTCTG	CGCTGGACAA
1401	AAACTATCGC	ATCGATGCCC	CCTGCCCGTA	CCTGCCCAAT	GCCTACGCCA
1451	ACACCGCCCA	CGGCACACGC	GGGCTTGCCA	CCGCCCCCAT	CTGCGCCGCC
1501	GCCGTTGCAG	CCGAAATCCT	AGGCTTGCCC	CATCCCCTCT	CAAAACGCCT
1551	GCGCCACGCC	CTACACCCCA	ACCGCGCCAT	CATCCGCGCC	ATCGTCAGAA
1601	GGAAGGATCT	AACCCCTTAA			

a212.pep						
1	MDNLAWNGIP	DIRTLDQ TIR	KHAHPLNLIV	CLPDNQIPNF	QTAQDASDAE	
51	CRLKHLRLDQA	TQCLQFDSIN	LIEHILPDVR	FWLVPPSRTR	RLHEHFHHIS	
101	WQTEAIPQTE	SKPDKPWFAL	PQTSEKQKPE	HILVIGAGIS	<u>GAATAHALAS</u>	
151	YGISVLTVEA	RKAAQAASGN	RQGLLYAKIS	PHDTEQTELL	LAGYGYTKRL	
201	LGHILPESET	WGGNGIHLN	YSRTEQQRNH	ELGLQKHNNH	LYRSITQAEA	
251	EKIAGIPLNT	PYAEPLCGLF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL	
301	TDISHDGEKW	IASTPNGTFT	ATHIIYCTGA	NSPYLPETNL	ATLPLRQIRG	
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGASFIP	NSSHTGWNEA	
401	EEASNRRQAL	HLNPALSESL	FAANPNPQKH	QGHAARICDS	PDHPLPLVGAL	
451	GDIAAMQQTQY	AKALDKNYR	IDAPCPYLPN	AYANTAHGTR	<u>GLATAPICAA</u>	
501	AVAAEILGLP	HPLSKRLRHA	LHPNRAIIRA	IVRRKDLTP*		

m212.pep MDNLVWDGIPDIRTLDOAIRKHAPLNLIICLPDNPQIPDFQTAAQDASDAECRLKHLRDLQA
|||||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
a212 MDNLAWNGIPDIRTLDQIRKHAPELNLIVCLPDNOIPIPFOTAADASDAECRLKHLRDLQA

491

	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPVSRTHHLHEHFHHISWQTEAIPQTESKPKDPWFAL					
a212	TQCLQFDSINLIEHILPDVRFWLVPVSRTRRLHEHFHHISWQTEAIPQTESKPKDPWFAL					
	130	140	150	160	170	180
m212.pep	PQTSEKQPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
a212	PQTSEKQPEHILVIGAGISGAATAHALASYGISVTVLEARKAAQAASGNRQGLLYAKIS					
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIHLNYSRTEQQRNHELGLQKHHNH					
a212	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIHLNYSRTEQQRNHELGLQKHHNH					
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYQHGVLNPPAFVRTLNNHPLIGLHEDTPL					
a212	LYRSITQAEAEKIAGIPLNTPYAEPLCGLFWQYGVWLNPPFTVRALLSHPLIGLHEDTPL					
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNLALPLRQIRGQTGLTPSTPF					
a212	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNLATLPLRQIRGQTGLTPSTPF					
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGFIPNSSHTGWNEAEASNRQALAHLPALSES					
a212	SEQLRCAVSGESYISPSWHGLHCYGFIPNSSHTGWNEAEASNRQALAHLPALSES					
	430	440	450	460	470	480
m212.pep	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN					
a212	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMQOTYAKLALDKNYRIDAPCPYLPN					
	490	500	510	520	530	540
m212.pep	AYVNTAHGTRGLATAPICAAXXAAQIXGLPHPFQRLRHALHPNRTIIRAIIVRRKDLTPX					
a212	AYANTAHGTRGLATAPICAAVAAEIIGLPHPLSKRLRHALHPNRAIIRAIIVRRKDLTPX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctatttgtt ttaattgtaa tttttgcaac
51  ttctcccgtt ttgccccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcttc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaa ggcaggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaagggtcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gtccagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

```

g214.pep

```

492

```

1  MIQKICKLVFV LIVIFATSPA FALQSDSRPP IQIEADQGS L DQANQRTTFS
51  GNVIIRQGT L NISASCVNVT RGRQRRRIE GGRFARPLQ NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRR RRCGHYLQHQ NRSLYHQHQH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTACAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGC GC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGCGCG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLVFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVIIRQGT L NISAARVNVT RGRQRRRIE GGRFASPLQ DIGRRQRHGA
101 RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQHQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214

      10      20      30      40      50      60
m214.pep  MIQKICKLVFLIAFFSASPALQSDSRQPIQIEADQGS LDQANQSTTFSGNVIRQGT L
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g214      MIQKICKLVFLIVIFATSPALQSDSRRP IQIEADQGS LDQANQRTTFSGNVIRQGT L
          10      20      30      40      50      60

      70      80      90      100     110     120
m214.pep  NISAARVNVTGRQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRCLFICRQHRSLNRX
          |||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
g214      NISASCVNVTGRQRRRIREGGRFARPLQPNVGRGQRD GARS GKQRYLFLRRKHCRSDRQ
          70      80      90      100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRCGDYIQHQNRSLYHQHQHKI
          |||: |||| |:|||||:|||||:|||||:|
g214      CQSAARRRCRRRCGHYLQHQNRSLYHQHQEIGCEIRFQNRQGQRRHPAFKHTKNRITPM
          130     140     150     160     170     180

g214      PSETETQFRRHLPTMPRRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTACAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGGCGGCG AATCCGTGAG GCGGGAAGGT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

493

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISAARVNVT RGXQRRRIE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLF I CRQHRSLNR* CQSTARRRC R RCGDYIQH Q NRSLYHQ RQH
151 KIRRKIRFQ I RQGQRRYPAF EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
a214	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
	10	20	30	40	50	60
m214.pep	NISAARVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNR X					
a214	NISAARVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNR X					
	70	80	90	100	110	120
m214.pep	NISAARVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNR X					
a214	NISAARVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNR X					
	70	80	90	100	110	120
m214.pep	CQSTARRRC RRCGDYIQH QNRSLYHQ RQH KI					
a214	CQSTARRRC RRCGDYIQH QNRSLYHQ RQH KIRRKIRFQ I RQGQRRYPAF EYAKIRIIP M					
	130	140	150	160	170	180
a214	PSETXTWFG R HLPTEILKRY L X					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTGC AAC
 51 TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTTCCG CCTCGCGCGT
201 CAACGTCACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTACGCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCTCTC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CCGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISASRVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVTYSS AGSTVVLGN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGCG
 51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT

```

m214-1.pgp

```

1      MIQKICKLFV  LIAFFSASPA  FALQSDSRQP  IQIEADQGS L  DQANQSTTFS
51     GNVVIRGTL  NISAARVNT  RGGKGGESVR  AEGSPVRF S Q  TLDGKGKGV R
101    QGANNVAYS  AGSTVLTGN  AKVQRGGDVA  EGAVITYN T K  TEVYTI S GST
151    KSGAKSASKS  GRVSVVLPS  STOKES*

```

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFLVLI	AFFSASP	AFALQSD	SRPQIEAD	QGS	LDQANQSTTFSGNVVIRQ
g214-1	MIQKICKLFLVLI	VIFATSP	AFALQSD	SRRPQIEAD	QGS	LDQANQSTTFSGNVVIRQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m214-1.pep	NISAARVNV	TRGGK	GGESV	RAEGSP	VRFSQ	TLDDGKG
g214-1	NISASRVNV	TRGGK	GGESV	RAEGSP	VRFSQ	TLDDGKG
	70	80	90	100	110	120
	130	140	150	160	170	
m214-1.pep	AKVQRGGD	VAEGAVI	TYNTKTE	VYTTISG	STKSGAK	SAKSGRVS
g214-1	AKVQRGGD	VAEGAVI	TYNTKTE	VYTTING	STKSGAK	SAKSGRVS
	130	140	150	160	170	

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_ol85 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

```

Query: 19  PAFALQSDSRQPIQIEADQGSLLDQANQSTTFSGNVVIRQGTNLNISAARVNVTR--GGKGG 76
          PAF+  D+  QPI IE+DQ SLD      TF+GNV++ QGT+ I+A +V VTR  G +G
Sbjct: 24  PAFAVTGDTDQPIHIESDQQSLDMQGNVVTFTGNVIVTQGTIKINADKVVVTRPGEQGG 83

Query: 77  ESVRAEGSPVRFQSQTLDGGKGTVRGQANNVAYSSAGSTVVLTGNAKVQRGGDVAEGAVIT 136
          E +   G P  F Q  D GK  V G A+ + Y A  VVLTGNA +Q+   +G IT
Sbjct: 84  EVIDGYGKPATFYQMQDNGK-PVEGHASQMHYELAKDFVVLVTGNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142
          Y  K +
Sbjct: 143 YLVKEQ 148

```

a214-1.seq

1	ATGATACAAA	AGATATGTAA	GCTATTGTGT	TTAATAGCAT	TTTTTTCGGC
51	GTCGCCCGCT	TTTGCCCTTC	AAAGCGGACAG	CAGGCAGCCT	ATTTCAGATTG
101	AGGCCGACCA	AGGTTTCGCT	GATCAAGCCA	ACCAAAAGCAC	CACATTTCAGC
151	AGGAACGTCG	TATCATGACA	GGGTACGCTC	AATATTTCGC	CGCGCCGCGT
201	CAATGTTACA	CGCGGCGGCA	AAGGCGGCGA	ATCCGTGAGG	CGGGAAGGTT
251	CGCCAGCTCG	CTTCACGCCG	ACATTGGACG	CGCGCAAAAG	CACGGTTCGCC
301	GGACAGGCCA	ACAACGTTCG	TATTTCATCT	GCAGGCAGCA	CCGTAGTCTT
351	AACCGGTAAT	GCCAAAGTAC	AGCGCGGCGG	CGATGTCGCC	GAAGGTGCGG
401	TGATTACATA	CAACACCAA	ACCGAAGTCT	ATACCATCAG	CGGCAGCAC
451	AAATCCGGCG	CAAAATCCGC	TTCCAAATCC	GGCAGGGTCA	CGGTCGTTAT
501	CCAGCCTTCG	AGTACGCAAA	AATCCGAATA	A	

a214-1.pwp

1 MIQKICKLFV LIAFFSASPA FALQSDSROP IOIEADOGSL DOANOSTTFS

495

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR
 101 GQANNVAYSS AGSTVVLGTN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKL	FVLIAFFS	SASPAFAL	QSDSRQPI	QIEADQGS	LDQANQSTTF
m214-1	MIQKICKL	FVLIAFFS	SASPAFAL	QSDSRQPI	QIEADQGS	LDQANQSTTF
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVN	VTTRGGK	GGESVRA	EGSPVRF	SQTLDGG	KGTVRGQAN
m214-1	NISAARVN	VTTRGGK	GGESVRA	EGSPVRF	SQTLDGG	KGTVRGQAN
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGG	DVAEGA	VITYNTK	TEVYTIS	GSTKSGA	KSASKSGR
m214-1	AKVQRGG	DVAEGA	VITYNTK	TEVYTIS	GSTKSGA	KSASKSGR
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq

```

1  atgaaagtaa gatggcggtta cggaaattgcg ttccattga tattggcggt
51  tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
151 ttggacggaa ggcggtttga cgaacaggga tacttgaaag aacatttgag
201 cgcgaaaggt gcgaaacagt ttccgaaaa cagcgacatc cattttgatt
251 cgccgcattc cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
301 agcgatgaag cgttttacca taccgaaaac aaacagggttc tttttaaaaa
351 caacgtttgt ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaaag
401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
451 gatacgcttg tcagtttcca atatggcgcg tcgcacggtc aggcggggcg
501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
551 aagccgcgat ttatgataca aaagatatgt aa

```

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep

```

1  MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
51  LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYEVG
101 SDEAVYHTEN KQVLFKNVNV LTKTADGRRQ AGKVETEKLH VDTESQYAQT
151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)

```

1  ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
51  CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC
151 GCGAAACAGT TTCCGAAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
201 CGTGTCTTCTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTTGTG
301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC
451 GACCACAwA CAGGCATGTT GAACTTCTCA TCTAAAGTGA AAGCCACGAT
501 TTATGATACA AAAGATATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)

```

1  ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
51  AKQFPESDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNVNV
101 LTKTADGKRQ AGKVEAEKLH VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

```

496

151 DHXTGMLNFS SKVKATIIDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
		:				
g215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTM	DGLD	GRRFDEQG		
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQ	EGRLLYEVGS	DEAVYHTENKQVLFKNNVV	
	:					
g215	YLKEHLSAKGAKQFP	ENS	DIHFDS	PHLVFFQ	EGRLLYEVGS	
	70	80	90	100	110	
	110	120	130	140	150	
m215.pep	LTKTADGKRQAGK	VEAEKLHVD	TESQYAQT	DPV	SFQYGASHGQAGGMTYDHXTGMLNFS	
	:					
g215	LTKTADGRRQAGK	VETEK	LHVD	TESQYAQT	DPV	
	130	140	150	160	170	
	170					
m215.pep	SKVKATIIDTKDMX					
	:					
g215	SKVKAATIIDTKDM					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq	
1	ATGAAAGTAA GATGGCGGTA CGGAATTGCG TTCCCATTTGA TATTGGCGGT
51	TGCCTTGGGC AGCCTGTCTG CATGGTTGGG ACGCATCAGC GAAGTCGAGA
101	TTGAAGAAGT CAGGCTCAAT CCGACGAAC CGCAATACAC AATGGACGGA
151	TTGGATGGCA GCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG
201	TTCGAAGGCG GCGAAACAGT TTCCCGAAAG CAGCGACATT CATTTCGACT
251	CACCGCATCT CGTGTCTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC
301	AGCGATGAAG CCGTTTACCA TACCGAAAAC AAACAGGTC TTTTAAAAA
351	CAACGTTGTG CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG
401	TTGAAGCCGA AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC
451	GATACGCTG TCAGTTTCCA ATATGGTGCA TCGCACGTC AGGCGGGCGG
501	CATGACTTAC GACCACAAA CAGGCATGTT GAACCTCTCA TCTAAAGTGA
551	AAGCCACGAT TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep	
1	MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTM
51	LDGRRFDEQG YLKEHLSSKG AKQFPESDI HFDS
101	SDEAVYHTEN KQVLFKNNVV LTKTADGKRQ AGKVEAEKLH VDESQYAQT
151	DPV

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
		:				
a215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTM	DGLD	GRRFDEQG		
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQ	EGRLLYEVGS	DEAVYHTENKQVLFKNNVV	

497

```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
              70      80      90      100      110      120

              110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
              130      140      150      160      170      180

              170
m215.pep  SKVKATIYDTKDMX
              |||||
a215      SKVKATIYDTKDMX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

```

g216.seq (partial)
1  ..atgatatcga tttcgagctc ggtacccagc gacgaaatca cgcctcatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcate accgcccgcg
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgcgctg tgccgacatt atgcacaaag gcggcgccct
351 gcccgccgct cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaaag tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt ttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

```

g216.pep (partial)
1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGAI VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

```

m216.seq
1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGT
51  GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGsACAAAA
101 ACTTCGTCTT TGCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCG TCctGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTTCG CTTGAGCCAT CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGCG
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGCGGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

```

m216.pep
1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

498

```

51  ITGMVKSGHI  GRKMAATMAS  TGTPAFFVHP  AEAHGDLM  IVDXDVVVAI
101 SNSGESDEIA  AIIPALKRKD  ITLVCITARP  DSTMARHADI  HITASVSKEA
151 CPLGLAPPTS  TTAVMALGDA  LAVVLLRARA  FTPDDFALSH  PAGSLGKRL
201 LRVADIMHKG  GGLPAVRLGT  PLKEAIVSMS  EKGLGMLAVT  DGQGRLLKGVF
251 TDGDLRRLFQ  ECDNFTGLSI  DEVMHHPKT  ISAERLATEA  LKVMQANHVN
301 GLLVTDADGV  LIGALNMHDL  LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100      110      120
m216.pep      TMASTGTPAFFVHPAEAAHGDLMIVDXDVVAISNSGESDEIAAIIPALKRKDITLVC
              ::|||:|  ||||:|||||
g216           MISISSVPSDEITAIIPALKRKDITLVC
              10      20      30

              130     140     150     160     170     180
m216.pep      TARPDMSTARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              |||||:|||||
g216           TARPDMSTARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              40      50      60      70      80      90

              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPKEAIVSMSEKGLGMLAVTDGQGR
              |||||:|||||
g216           ALIHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPKGAIVSMSEKGLGMWAGTDGQR
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

```

a216.seq
1  ATGGCGATGG  CAGGAAACGA  AAAATATCTT  GATTGGGCAC  GCGAAGTGTT
51  GCACACCGAA  GCGGAAGGCT  TCGCGCGAAT  TCGCGCGGAT  TTGGACGAAA
101 ACTTCGCCCT  TCGCGCGGAC  GCGTTGTTGC  ACTGCAAAGG  CAGGGTCGTT
151 ATCACGGGCA  TGGGCAAGTC  GGGACATATC  GGGCGCAAAA  TGGCGGCAAC
201 CATGGCCTCG  ACCGGCACGC  CCGCGTTTTC  CGTCCACCCT  GCGGAAGCGG
251 CACACGGCGA  TTTGGGCATG  ATTGTGGACA  ACGACGTGGT  CGTCGCGATT
301 TCCAATTCCG  GTGAAAGCGA  CGAAATCGCC  GCCATCATCC  CCGCGCTCAA
351 ACGCAAAGAT  ATCACGCTTG  TCTGCATCAC  CGCCCGCCCC  GATTCAACCA
401 TGGCGCGCCA  TGCCGACATC  CACATCACGG  CGTCGGTTTC  CAAAGAAGCC
451 TGCCCGCTGG  GGCTTGCCCC  GACCACCAGC  ACCACCGCCG  TTATGGCTTT
501 GGGCGATGCG  TTGGCGGTTG  TCCTGCTGCG  CGCCCGCGCG  TTCACGCCCG
551 ACGACTTCGC  CTTGAGCCAC  CCTGCCGGCA  GCCTCGGCAA  ACGCCTACTT
601 TTGCGCGTTG  CCGACATTAT  GCACAAAGGC  GCGCGCCTGC  CTGCCGTCGG
651 ACTCGGCACG  CCCTTGAAAG  AAGCCATCGT  CAGCATGAGT  GAAAAAGGGC
701 TGGGCATGTT  GGCGGTAACG  GACGGGCAAG  GCCGTCTGAA  AGGCGTATTC
751 ACCGACGGCG  ATTTGCGCCG  CCTGTTTCAA  GAATGCGACA  ATTTTACCGG
801 TCTTTCGATA  GACGAAGTCA  TGCATACGCA  TCCTAAAACC  ATCTCCGCCG
851 AACGTCTCGC  CACCGAAGCC  CTGAAAGTCA  TGCAGGCAAA  CCATGTGAAC
901 GGGCTTCTGG  TTACCGATGC  AGATGGCGTG  CTGATCGGCG  CGCTGAATAT
951 GCACGACCTT  TTGGCGGCGC  GGATTGTATA  G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

```

a216.pep
1  MAMAGNEKYL  DWAREVLHTE  AEGLEIAAD  LDENFALAAD  ALLHCKGRVV
51  ITGMVKSGHI  GRKMAATMAS  TGTPAFFVHP  AEAHGDLM  IVDNDVVVAI
101 SNSGESDEIA  AIIPALKRKD  ITLVCITARP  DSTMARHADI  HITASVSKEA
151 CPLGLAPPTS  TTAVMALGDA  LAVVLLRARA  FTPDDFALSH  PAGSLGKRL
201 LRVADIMHKG  GGLPAVRLGT  PLKEAIVSMS  EKGLGMLAVT  DGQGRLLKGVF
251 TDGDLRRLFQ  ECDNFTGLSI  DEVMHHPKT  ISAERLATEA  LKVMQANHVN

```


499

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENGKYL	DWAREVLHAE	AEGLREIAAE	LXKNFVLAAD	ALLHCKGRVV	ITGMVKS
a216	MAMAGNEKYL	DWAREVLHTE	AEGLREIAAD	LDENFALAAD	ALLHCKGRVV	ITGMGKS
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMA	STGTPAFFV	HPAEAAHGD	LGMIVDXDV	VVAISNSGE	SDEIAAII
a216	GRKMAATMA	STGTPAFFV	HPAEAAHGD	LGMIVDNDV	VVAISNSGE	SDEIAAII
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITAR	PDSTMARHAD	IHITASVSKE	ACPLGLAPT	TSTTAVMAL	GDALAVVLR
a216	ITLVCITAR	PDSTMARHAD	IHITASVSKE	ACPLGLAPT	TSTTAVMAL	GDALAVVLR
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFAL	SHPAGSLGK	RLLLRVADIM	HKGGGLPAV	RLGTPLKEA	IVSMSEKGL
a216	FTPDDFAL	SHPAGSLGK	RLLLRVADIM	HKGGGLPAV	RLGTPLKEA	IVSMSEKGL
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRILK	GVFTDGLR	RLRFQECDF	TGLSIDEVM	HTHPKTISA	ERLATEALK
a216	DGQGRILK	GVFTDGLR	RLRFQECDF	TGLSIDEVM	HTHPKTISA	ERLATEALK
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADG	VLIGALNMH	DLLAARIVX			
a216	GLLVTDADG	VLIGALNMH	DLLAARIVX			
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttgtt gcggcaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttcgaggtt ttggactgcc
101 ttttggtcac cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgcagg ttgccgccat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcgggt
251 tgattcacgt cggcatacca cgcgctgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatccccaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcag aaacggcgca acacgggcgc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttcagca agtcggacac gactccaac
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgtata ggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVOKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAFOQQVGH ALQRIKKRLP AADFHVRNGI

```

500

201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG ACGGTGTGCG GCGGCAACTG TCCGAAAAAT TGCGCCAATT
51  CGGTTTCCGC CTrCCATTG ACCCATTCGT TTTCAAGGTT TTGGACTGAC
101 TTTTGGTCAT CGGCTTCAGC TTGGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTCCCGCA CCGTTGCGGG CTGCCGCCAT ATCCGTACAA
201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CATGGCGGTT
251 TGATTACAGT CGGCATACCA CGCGCTGACA TCCTGCCACA TCGGATTGCC
301 GCCTTTGGGC AGCATCCAGC CCAATATCAT GCGTTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 TGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGTA AATCGTCCTC
451 AGTCAGTCCG AAACGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGGCG GCGGCTGATT TTCACGTCGT ACACGGAATA
601 CGGCAATGCC TGCGCACCgG GctGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL SGKLRQFGFR LPFDPFVFKV LDXLLVIGFS LEQCFKQIPA
51  TRHPFADRCG LPPYPYNIQ GFEEGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLPGEQ LIRAAAHFSV QTPVDVQIGN HVVQKRXIVL
151 SQSETAQHGR GFXXKHKFID FKSAPQVEQ AXQSMKQRLA AADFHVXHGI
201 RQCLRTGLRL SEHGFDKRII GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHPPFADRCG					
g217	MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHPPFADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIQGFEEGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLPGEQ					
g217	LPPYPGNIRQGFEEGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFXXKHKFIDFKSAFQQVEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKQIVPGQSETAQHGRGFQKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRII GFDIRGX					
g217	ALQRIKKRLPAADFHVRNGIRQCLRAGLRLSEHGFKRRI GFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAAT TGCGCCAATT
51  CGGTTTCCGC CTGCCATTG ACCCATTCGT TTTGAGGCT TTGGACTGCC
101 TTTTGGTCAT CGCCTTCGAC TTGGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTCTCAA CCGTCGAGG TTGCCGCCAT ATCCGTACAA

```